



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Ken Stokes
Josée Morissette
- (ii) TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL
SENSING BY CARDIAC PACEMAKERS THROUGH
GENETIC TREATMENT
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris LLP
 - (B) STREET: One Liberty Place - 46th Floor
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WordPerfect 6.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: N/A
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Paul K. Legaard
 - (B) REGISTRATION NUMBER: 38,534
 - (C) REFERENCE/DOCKET NUMBER: MEDT-0082
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (215) 568-3100
 - (B) TELEFAX: (215) 568-3439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6048 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	GCA	AAC	TTC	CTA	TTA	CCT	CGG	GGC	ACC	AGC	AGC	TTC	CGC	AGG	45
Met	Ala	Asn	Phe	Leu	Leu	Pro	Arg	Gly	Thr	Ser	Ser	Phe	Arg	Arg	
1				5				10						15	
TTC	ACA	CGG	GAG	TCC	CTG	GCA	GCC	ATC	GAG	AAG	CGC	ATG	GCG	GAG	90
Phe	Thr	Arg	Glu	Ser	Leu	Ala	Ala	Ile	Glu	Lys	Arg	Met	Ala	Glu	
			20					25						30	
AAG	CAA	GCC	CGC	GGC	TCA	ACC	ACC	TTG	CAG	GAG	AGC	CGA	GAG	GGG	135
Lys	Gln	Ala	Arg	Gly	Ser	Thr	Thr	Leu	Gln	Glu	Ser	Arg	Glu	Gly	
			35					40						45	

CTG	CCC	GAG	GAG	GAG	GCT	CCC	CGG	CCC	CAG	CTG	GAC	CTG	CAG	GCC	180
Leu	Pro	Glu	Glu	Glu	Ala	Pro	Arg	Pro	Gln	Leu	Asp	Leu	Gln	Ala	
				50					55					60	
TCC	AAA	AAG	CTG	CCA	GAT	CTC	TAT	GGC	AAT	CCA	CCC	CAA	GAG	CTC	225
Ser	Lys	Lys	Leu	Pro	Asp	Leu	Tyr	Gly	Asn	Pro	Pro	Gln	Glu	Leu	
				65					70					75	
ATC	GGA	GAG	CCC	CTG	GAG	GAC	CTG	GAC	CCC	TTC	TAT	AGC	ACC	CAA	270
Ile	Gly	Glu	Pro	Leu	Glu	Asp	Leu	Asp	Pro	Phe	Tyr	Ser	Thr	Gln	
				80					85					90	
AAG	ACT	TTC	ATC	GTA	CTG	AAT	AAA	GGC	AAG	ACC	ATC	TTC	CGG	TTC	315
Lys	Thr	Phe	Ile	Val	Leu	Asn	Lys	Gly	Lys	Thr	Ile	Phe	Arg	Phe	
				95					100					105	
AGT	GCC	ACC	AAC	GCC	TTG	TAT	GTC	CTC	AGT	CCC	TTC	CAC	CCA	GTT	360
Ser	Ala	Thr	Asn	Ala	Leu	Tyr	Val	Leu	Ser	Pro	Phe	His	Pro	Val	
				110					115					120	
CGG	AGA	GCG	GCT	GTG	AAG	ATT	CTG	GTT	CAC	TCG	CTC	TTC	AAC	ATG	405
Arg	Arg	Ala	Ala	Val	Lys	Ile	Leu	Val	His	Ser	Leu	Phe	Asn	Met	
				125					130					135	
CTC	ATC	ATG	TGC	ACC	ATC	CTC	ACC	AAC	TGC	GTG	TTC	ATG	GCC	CAG	450
Leu	Ile	Met	Cys	Thr	Ile	Leu	Thr	Asn	Cys	Val	Phe	Met	Ala	Gln	
				140					145					150	
CAC	GAC	CCT	CCA	CCC	TGG	ACC	AAG	TAT	GTC	GAG	TAC	ACC	TTC	ACC	495
His	Asp	Pro	Pro	Pro	Trp	Thr	Lys	Tyr	Val	Glu	Tyr	Thr	Phe	Thr	
				155					160					165	
GCC	ATT	TAC	ACC	TTT	GAG	TCT	CTG	GTC	AAG	ATT	CTG	GCT	CGA	GCT	540
Ala	Ile	Tyr	Thr	Phe	Glu	Ser	Leu	Val	Lys	Ile	Leu	Ala	Arg	Ala	
				170					175					180	
TTC	TGC	CTG	CAC	GCG	TTC	ACT	TTC	CTT	CGG	GAC	CCA	TGG	AAC	TGG	585
Phe	Cys	Leu	His	Ala	Phe	Thr	Phe	Leu	Arg	Asp	Pro	Trp	Asn	Trp	
				185					190					195	
CTG	GAC	TTT	AGT	GTG	ATT	ATC	ATG	GCA	TAC	ACA	ACT	GAA	TTT	GTG	630
Leu	Asp	Phe	Ser	Val	Ile	Ile	Met	Ala	Tyr	Thr	Thr	Glu	Phe	Val	
				200					205					210	
GAC	CTG	GGC	AAT	GTC	TCA	GCC	TTA	CGC	ACC	TTC	CGA	GTC	CTC	CGG	675
Asp	Leu	Gly	Asn	Val	Ser	Ala	Leu	Arg	Thr	Phe	Arg	Val	Leu	Arg	
				215					220					225	
GCC	CTG	AAA	ACT	ATA	TCA	GTC	ATT	TCA	GGG	CTG	AAG	ACC	ATC	GTG	720
Ala	Leu	Lys	Thr	Ile	Ser	Val	Ile	Ser	Gly	Leu	Lys	Thr	Ile	Val	
				230					235					240	
GGG	GCC	CTG	ATC	CAG	TCT	GTG	AAG	AAG	CTG	GCT	GAT	GTG	ATG	GTC	765
Gly	Ala	Leu	Ile	Gln	Ser	Val	Lys	Lys	Leu	Ala	Asp	Val	Met	Val	
				245					250					255	
CTC	ACA	GTC	TTC	TGC	CTC	AGC	GTC	TTT	GCC	CTC	ATC	GGC	CTG	CAG	810
Leu	Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Ile	Gly	Leu	Gln	
				260					265					270	

CTC	TTC	ATG	GGC	AAC	CTA	AGG	CAC	AAG	TGT	GTG	CGC	AAC	TTC	ACA	855
Leu	Phe	Met	Gly	Asn	Leu	Arg	His	Lys	Cys	Val	Arg	Asn	Phe	Thr	
				275					280					285	
GCG	CTC	AAC	GGC	ACC	AAC	GGC	TCC	GTG	GAG	GCC	GAC	GGC	TTG	GTC	900
Ala	Leu	Asn	Gly	Thr	Asn	Gly	Ser	Val	Glu	Ala	Asp	Gly	Leu	Val	
				290					295					300	
TGG	GAA	TCC	CTG	GAC	CTT	TAC	CTC	AGT	GAT	CCA	GAA	AAT	TAC	CTG	945
Trp	Glu	Ser	Leu	Asp	Leu	Tyr	Leu	Ser	Asp	Pro	Glu	Asn	Tyr	Leu	
				305					310					315	
CTC	AAG	AAC	GGC	ACC	TCT	GAT	GTG	TTA	CTG	TGT	GGG	AAC	AGC	TCT	990
Leu	Lys	Asn	Gly	Thr	Ser	Asp	Val	Leu	Leu	Cys	Gly	Asn	Ser	Ser	
				320					325					330	
GAC	GCT	GGG	ACA	TGT	CCG	GAG	GGC	TAC	CGG	TGC	CTA	AAG	GCA	GGC	1035
Asp	Ala	Gly	Thr	Cys	Pro	Glu	Gly	Tyr	Arg	Cys	Leu	Lys	Ala	Gly	
				335					340					345	
GAG	AAC	CCC	GAC	CAC	GGC	TAC	ACC	AGC	TTC	GAT	TCC	TTT	GCC	TGG	1080
Glu	Asn	Pro	Asp	His	Gly	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Ala	Trp	
				350					355					360	
GCC	TTT	CTT	GCA	CTC	TTC	CGC	CTG	ATG	ACG	CAG	GAC	TGC	TGG	GAG	1125
Ala	Phe	Leu	Ala	Leu	Phe	Arg	Leu	Met	Thr	Gln	Asp	Cys	Trp	Glu	
				365					370					375	
CGC	CTC	TAT	CAG	CAG	ACC	CTC	AGG	TCC	GCA	GGG	AAG	ATC	TAC	ATG	1170
Arg	Leu	Tyr	Gln	Gln	Thr	Leu	Arg	Ser	Ala	Gly	Lys	Ile	Tyr	Met	
				380					385					390	
ATC	TTC	TTC	ATG	CTT	GTC	ATC	TTC	CTG	GGG	TCC	TTC	TAC	CTG	GTG	1215
Ile	Phe	Phe	Met	Leu	Val	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	
				395					400					405	
AAC	CTG	ATC	CTG	GCC	GTG	GTC	GCA	ATG	GCC	TAT	GAG	GAG	CAA	AAC	1260
Asn	Leu	Ile	Leu	Ala	Val	Val	Ala	Met	Ala	Tyr	Glu	Glu	Gln	Asn	
				410					415					420	
CAA	GCC	ACC	ATC	GCT	GAG	ACC	GAG	GAG	AAG	GAA	AAG	CGC	TTC	CAG	1305
Gln	Ala	Thr	Ile	Ala	Glu	Thr	Glu	Glu	Lys	Glu	Lys	Arg	Phe	Gln	
				425					430					435	
GAG	GCC	ATG	GAA	ATG	CTC	AAG	AAA	GAA	CAC	GAG	GCC	CTC	ACC	ATC	1350
Glu	Ala	Met	Glu	Met	Leu	Lys	Lys	Glu	His	Glu	Ala	Leu	Thr	Ile	
				440					445					450	
AGG	GGT	GTG	GAT	ACC	GTG	TCC	CGT	AGC	TCC	TTG	GAG	ATG	TCC	CCT	1395
Arg	Gly	Val	Asp	Thr	Val	Ser	Arg	Ser	Ser	Leu	Glu	Met	Ser	Pro	
				455					460					465	
TTG	GCC	CCA	GTA	AAC	AGC	CAT	GAG	AGA	AGA	AGC	AAG	AGG	AGA	AAA	1440
Leu	Ala	Pro	Val	Asn	Ser	His	Glu	Arg	Arg	Ser	Lys	Arg	Arg	Lys	
				470					475					480	
CGG	ATG	TCT	TCA	GGA	ACT	GAG	GAG	TGT	GGG	GAG	GAC	AGG	CTC	CCC	1485
Arg	Met	Ser	Ser	Gly	Thr	Glu	Glu	Cys	Gly	Glu	Asp	Arg	Leu	Pro	
				485					490					495	
AAG	TCT	GAC	TCA	GAA	GAT	GGT	CCC	AGA	GCA	ATG	AAT	CAT	CTC	AGC	1520

Lys	Ser	Asp	Ser	Glu	Asp	Gly	Pro	Arg	Ala	Met	Asn	His	Leu	Ser	
				500					505					510	
CTC	ACC	CGT	GGC	CTC	AGC	AGG	ACT	TCT	ATG	AAG	CCA	CGT	TCC	AGC	1565
Leu	Thr	Arg	Gly	Leu	Ser	Arg	Thr	Ser	Met	Lys	Pro	Arg	Ser	Ser	
				515					520					525	
CGC	GGG	AGC	ATT	TTC	ACC	TTT	CGC	AGG	CGA	GAC	CTG	GGT	TCT	GAA	1620
Arg	Gly	Ser	Ile	Phe	Thr	Phe	Arg	Arg	Arg	Asp	Leu	Gly	Ser	Glu	
				530					535					540	
GCA	GAT	TTT	GCA	GAT	GAT	GAA	AAC	AGC	ACA	GCG	CGG	GAG	AGC	GAG	1665
Ala	Asp	Phe	Ala	Asp	Asp	Glu	Asn	Ser	Thr	Ala	Arg	Glu	Ser	Glu	
				545					550					555	
AGC	CAC	CAC	ACA	TCA	CTG	CTG	GTG	CCC	TGG	CCC	CTG	CGC	CGG	ACC	1710
Ser	His	His	Thr	Ser	Leu	Leu	Val	Pro	Trp	Pro	Leu	Arg	Arg	Thr	
				560					565					570	
AGT	GCC	CAG	GGA	CAG	CCC	AGT	CCC	GGA	ACC	TCG	GCT	CCT	GGC	CAC	1755
Ser	Ala	Gln	Gly	Gln	Pro	Ser	Pro	Gly	Thr	Ser	Ala	Pro	Gly	His	
				575					580					585	
GCC	CTC	CAT	GGC	AAA	AAG	AAC	AGC	ACT	GTG	GAC	TGC	AAT	GGG	GTG	1800
Ala	Leu	His	Gly	Lys	Lys	Asn	Ser	Thr	Val	Asp	Cys	Asn	Gly	Val	
				590					595					600	
GTC	TCA	TTA	CTG	GGG	GCA	GGC	GAC	CCA	GAG	GCC	ACA	TCC	CCA	GGA	1845
Val	Ser	Leu	Leu	Gly	Ala	Gly	Asp	Pro	Glu	Ala	Thr	Ser	Pro	Gly	
				605					610					615	
AGC	CAC	CTC	CTC	CGC	CCT	GTG	ATG	CTA	GAG	CAC	CCG	CCA	GAC	ACG	1890
Ser	His	Leu	Leu	Arg	Pro	Val	Met	Leu	Glu	His	Pro	Pro	Asp	Thr	
				620					625					630	
ACC	ACG	CCA	TCG	GAG	GAG	CCA	GGC	GGC	CCC	CAG	ATG	CTG	ACC	TCC	1935
Thr	Thr	Pro	Ser	Glu	Glu	Pro	Gly	Gly	Pro	Gln	Met	Leu	Thr	Ser	
				635					640					645	
CAG	GCT	CCG	TGT	GTA	GAT	GGC	TTC	GAG	GAG	CCA	GGA	GCA	CGG	CAG	1980
Gln	Ala	Pro	Cys	Val	Asp	Gly	Phe	Glu	Glu	Pro	Gly	Ala	Arg	Gln	
				650					655					660	
CGG	GCC	CTC	AGC	GCA	GTC	AGC	GTC	CTC	ACA	AGC	GCA	CTG	GAA	GAG	2025
Arg	Ala	Leu	Ser	Ala	Val	Ser	Val	Leu	Thr	Ser	Ala	Leu	Glu	Glu	
				665					670					675	
TTA	GAG	GAG	TCT	CGC	CAC	AAG	TGT	CCA	CCA	TGC	TGG	AAC	CGT	CTC	2070
Leu	Glu	Glu	Ser	Arg	His	Lys	Cys	Pro	Pro	Cys	Trp	Asn	Arg	Leu	
				680					685					690	
GCC	CAG	CGC	TAC	CTG	ATC	TGG	GAG	TGC	TGC	CCG	CTG	TGG	ATG	TCC	2115
Ala	Gln	Arg	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	Leu	Trp	Met	Ser	
				695					700					705	
ATC	AAG	CAG	GGA	GTG	AAG	TTG	GTG	GTC	ATG	GAC	CCG	TTT	ACT	GAC	2160
Ile	Lys	Gln	Gly	Val	Lys	Leu	Val	Val	Met	Asp	Pro	Phe	Thr	Asp	
				710					715					720	
CTC	ACC	ATC	ACT	ATG	TGC	ATC	GTA	CTC	AAC	ACA	CTC	TTC	ATG	GCG	2205
Leu	Thr	Ile	Thr	Met	Cys	Ile	Val	Leu	Asn	Thr	Leu	Phe	Met	Ala	

				725					730					735	
CTG	GAG	CAC	TAC	AAC	ATG	ACA	AGT	GAA	TTC	GAG	GAG	ATG	CTG	CAG	2250
Leu	Glu	His	Tyr	Asn	Met	Thr	Ser	Glu	Phe	Glu	Glu	Met	Leu	Gln	
				740					745					750	
GTC	GGA	AAC	CTG	GTC	TTC	ACA	GGG	ATT	TTC	ACA	GCA	GAG	ATG	ACC	2295
Val	Gly	Asn	Leu	Val	Phe	Thr	Gly	Ile	Phe	Thr	Ala	Glu	Met	Thr	
				755					760					765	
TTC	AAG	ATC	ATT	GCC	CTC	GAC	CCC	TAC	TAC	TAC	TTC	CAA	CAG	GGC	2340
Phe	Lys	Ile	Ile	Ala	Leu	Asp	Pro	Tyr	Tyr	Tyr	Phe	Gln	Gln	Gly	
				770					775					780	
TGG	AAC	ATC	TTC	GAC	AGC	ATC	ATC	GTC	ATC	CTT	AGC	CTC	ATG	GAG	2385
Trp	Asn	Ile	Phe	Asp	Ser	Ile	Ile	Val	Ile	Leu	Ser	Leu	Met	Glu	
				785					790					795	
CTG	GGC	CTG	TCC	CGC	ATG	AGC	AAC	TTG	TCG	GTG	CTG	CGC	TCC	TTC	2430
Leu	Gly	Leu	Ser	Arg	Met	Ser	Asn	Leu	Ser	Val	Leu	Arg	Ser	Phe	
				800					805					810	
CGC	CTG	CTG	CGG	GTC	TTC	AAG	CTG	GCC	AAA	TCA	TGG	CCC	ACC	CTG	2475
Arg	Leu	Leu	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	
				815					820					825	
AAC	ACA	CTC	ATC	AAG	ATC	ATC	GGG	AAC	TCA	GTG	GGG	GCA	CTG	GGG	2520
Asn	Thr	Leu	Ile	Lys	Ile	Ile	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	
				830					835					840	
AAC	CTG	ACA	CTG	GTG	CTA	GCC	ATC	ATC	GTG	TTC	ATC	TTT	GCT	GTG	2565
Asn	Leu	Thr	Leu	Val	Leu	Ala	Ile	Ile	Val	Phe	Ile	Phe	Ala	Val	
				845					850					855	
GTG	GGC	ATG	CAG	CTC	TTT	GGC	AAG	AAC	TAC	TCG	GAG	CTG	AGG	GAC	2610
Val	Gly	Met	Gln	Leu	Phe	Gly	Lys	Asn	Tyr	Ser	Glu	Leu	Arg	Asp	
				860					865					870	
AGC	GAC	TCA	GGC	CTG	CTG	CCT	CGC	TGG	CAC	ATG	ATG	GAC	TTC	TTT	2655
Ser	Asp	Ser	Gly	Leu	Leu	Pro	Arg	Trp	His	Met	Met	Asp	Phe	Phe	
				875					880					885	
CAT	GCC	TTC	CTA	ATC	ATC	TTC	CGC	ATC	CTC	TGT	GGA	GAG	TGG	ATC	2700
His	Ala	Phe	Leu	Ile	Ile	Phe	Arg	Ile	Leu	Cys	Gly	Glu	Trp	Ile	
				890					895					900	
GAG	ACC	ATG	TGG	GAC	TGC	ATG	GAG	GTG	TCG	GGG	CAG	TCA	TTA	TGC	2745
Glu	Thr	Met	Trp	Asp	Cys	Met	Glu	Val	Ser	Gly	Gln	Ser	Leu	Cys	
				905					910					915	
CTG	CTG	GTC	TTC	TTG	CTT	GTT	ATG	GTC	ATT	GGC	AAC	CTT	GTG	GTC	2790
Leu	Leu	Val	Phe	Leu	Leu	Val	Met	Val	Ile	Gly	Asn	Leu	Val	Val	
				920					925					930	
CTG	AAT	CTC	TTC	CTG	GCC	TTG	CTG	CTC	AGC	TCC	TTC	AGT	GCA	GAC	2835
Leu	Asn	Leu	Phe	Leu	Ala	Leu	Leu	Leu	Ser	Ser	Phe	Ser	Ala	Asp	
				935					940					945	
AAC	CTC	ACA	GCC	CCT	GAT	GAG	GAC	AGA	GAG	ATG	AAC	AAC	CTC	CAG	2880
Asn	Leu	Thr	Ala	Pro	Asp	Glu	Asp	Arg	Glu	Met	Asn	Asn	Leu	Gln	
				950					955					960	

CTG	GCC	CTG	GCC	CGC	ATC	CAG	AGG	GGC	CTG	CGC	TTT	GTC	AAG	CGG	2925
Leu	Ala	Leu	Ala	Arg	Ile	Gln	Arg	Gly	Leu	Arg	Phe	Val	Lys	Arg	
				965					970					975	
ACC	ACC	TGG	GAT	TTC	TGC	TGT	GGT	CTC	CTG	CGG	CAC	CGG	CCT	CAG	2970
Thr	Thr	Trp	Asp	Phe	Cys	Cys	Gly	Leu	Leu	Arg	His	Arg	Pro	Gln	
				980					985					990	
AAG	CCC	GCA	GCC	CTT	GCC	GCC	CAG	GGC	CAG	CTG	CCC	AGC	TGC	ATT	3015
Lys	Pro	Ala	Ala	Leu	Ala	Ala	Gln	Gly	Gln	Leu	Pro	Ser	Cys	Ile	
				995					1000					1005	
GCC	ACC	CCC	TAC	TCC	CCG	CCA	CCC	CCA	GAG	ACG	GAG	AAG	GTG	CCT	3060
Ala	Thr	Pro	Tyr	Ser	Pro	Pro	Pro	Pro	Glu	Thr	Glu	Lys	Val	Pro	
				1010					1015					1020	
CCC	ACC	CGC	AAG	GAA	ACA	CAG	TTT	GAG	GAA	GGC	GAG	CAA	CCA	GGC	3105
Pro	Thr	Arg	Lys	Glu	Thr	Gln	Phe	Glu	Glu	Gly	Glu	Gln	Pro	Gly	
				1025					1030					1035	
CAG	GGC	ACC	CCC	GGG	GAT	CCA	GAC	GCC	GTG	TGT	GTG	CCC	ATC	GCT	3150
Gln	Gly	Thr	Pro	Gly	Asp	Pro	Glu	Pro	Val	Cys	Val	Pro	Ile	Ala	
				1040					1045					1050	
GTG	GCC	GAG	TCA	GAC	ACA	GAT	GAC	CAA	GAA	GAG	GAT	GAG	GAG	AAC	3195
Val	Ala	Glu	Ser	Asp	Thr	Asp	Asp	Gln	Glu	Glu	Asp	Glu	Glu	Asn	
				1055					1060					1065	
AGC	CTG	GGC	ACG	GAG	GAG	GAG	TCC	AGC	AAG	CAG	CAG	GAA	TCC	CAG	3240
Ser	Leu	Gly	Thr	Glu	Glu	Glu	Ser	Ser	Lys	Gln	Gln	Glu	Ser	Gln	
				1070					1075					1080	
CCT	GTG	TCC	GGC	TGG	CCC	AGA	GGC	CCT	CCG	GAT	TCC	AGG	ACC	TGG	3285
Pro	Val	Ser	Gly	Trp	Pro	Arg	Gly	Pro	Pro	Asp	Ser	Arg	Thr	Trp	
				1085					1090					1095	
AGC	CAG	GTG	TCA	GCG	ACT	GCC	TCC	TCT	GAG	GCC	GAG	GCC	AGT	GCA	3330
Ser	Gln	Val	Ser	Ala	Thr	Ala	Ser	Ser	Glu	Ala	Glu	Ala	Ser	Ala	
				1100					1105					1110	
TCT	CAG	GCC	GAC	TGG	CGG	CAG	CAG	TGG	AAA	GCG	GAA	CCC	CAG	GCC	3375
Ser	Gln	Ala	Asp	Trp	Arg	Gln	Gln	Trp	Lys	Ala	Glu	Pro	Gln	Ala	
				1115					1120					1125	
CCA	GGG	TGC	GGT	GAG	ACC	CCA	GAG	GAC	AGT	TGC	TCC	GAG	GGC	AGC	3420
Pro	Gly	Cys	Gly	Glu	Thr	Pro	Glu	Asp	Ser	Cys	Ser	Glu	Gly	Ser	
				1130					1135					1140	
ACA	GCA	GAC	ATG	ACC	AAC	ACC	GCT	GAG	CTC	CTG	GAG	CAG	ATC	CCT	3465
Thr	Ala	Asp	Met	Thr	Asn	Thr	Ala	Glu	Leu	Leu	Glu	Gln	Ile	Pro	
				1145					1150					1155	
GAC	CTC	GGC	CAG	GAT	GTC	AAG	GAC	CCA	GAG	GAC	TGC	TTC	ACT	GAA	3510
Asp	Leu	Gly	Gln	Asp	Val	Lys	Asp	Pro	Glu	Asp	Cys	Phe	Thr	Glu	
				1160					1165					1170	
GGC	TGT	GTC	CGG	CGC	TGT	CCC	TGC	TGT	GCG	GTG	GAC	ACC	ACA	CAG	3555
Gly	Cys	Val	Arg	Arg	Cys	Pro	Cys	Cys	Ala	Val	Asp	Thr	Thr	Gln	
				1175					1180					1185	

GCC	CCA	GGG	AAG	GTC	TGG	TGG	CGG	TTG	CGC	AAG	ACC	TGC	TAC	CAC	3600
Ala	Pro	Gly	Lys	Val	Trp	Trp	Arg	Leu	Arg	Lys	Thr	Cys	Tyr	His	
				1190					1195					1200	
ATC	GTG	GAG	CAC	AGC	TGG	TTC	GAG	ACA	TTC	ATC	ATC	TTC	ATG	ATC	3645
Ile	Val	Glu	His	Ser	Trp	Phe	Glu	Thr	Phe	Ile	Ile	Phe	Met	Ile	
				1205					1210					1215	
CTA	CTC	AGC	AGT	GGA	GCG	CTG	GCC	TTC	GAG	GAC	ATC	TAC	CTA	GAG	3690
Leu	Leu	Ser	Ser	Gly	Ala	Leu	Ala	Phe	Glu	Asp	Ile	Tyr	Leu	Glu	
				1220					1225					1230	
GAG	CGG	AAG	ACC	ATC	AAG	GTT	CTG	CTT	GAG	TAT	GCC	GAC	AAG	ATG	3735
Glu	Arg	Lys	Thr	Ile	Lys	Val	Leu	Leu	Glu	Tyr	Ala	Asp	Lys	Met	
				1235					1240					1245	
TTC	ACA	TAT	GTC	TTC	GTG	CTG	GAG	ATG	CTG	CTC	AAG	TGG	GTG	GCC	3780
Phe	Thr	Tyr	Val	Phe	Val	Leu	Glu	Met	Leu	Leu	Lys	Trp	Val	Ala	
				1250					1255					1260	
TAC	GGC	TTC	AAG	AAG	TAC	TTC	ACC	AAT	GCC	TGG	TGC	TGG	CTC	GAC	3825
Tyr	Gly	Phe	Lys	Lys	Tyr	Phe	Thr	Asn	Ala	Trp	Cys	Trp	Leu	Asp	
				1265					1270					1275	
TTC	CTC	ATC	GTA	GAC	GTG	TCT	CTG	GTC	AGC	CTG	GTG	GCC	AAC	ACC	3870
Phe	Leu	Ile	Val	Asp	Val	Ser	Leu	Val	Ser	Leu	Val	Ala	Asn	Thr	
				1280					1285					1290	
CTG	GGC	TTT	GCC	GAG	ATG	GGC	CCC	ATC	AAG	TCA	CTG	CGG	ACG	CTG	3915
Leu	Gly	Phe	Ala	Glu	Met	Gly	Pro	Ile	Lys	Ser	Leu	Arg	Thr	Leu	
				1295					1300					1305	
CGT	GCA	CTC	CGT	CCT	CTG	AGA	GCT	CTG	TCA	CGA	TTT	GAG	GGC	ATG	3960
Arg	Ala	Leu	Arg	Pro	Leu	Arg	Ala	Leu	Ser	Arg	Phe	Glu	Gly	Met	
				1310					1315					1320	
AGG	GTG	GTG	GTC	AAT	GCC	CTG	GTG	GGC	GCC	ATC	CCG	TCC	ATC	ATG	4005
Arg	Val	Val	Val	Asn	Ala	Leu	Val	Gly	Ala	Ile	Pro	Ser	Ile	Met	
				1325					1330					1335	
AAC	GTC	CTC	CTC	GTC	TGC	CTC	ATC	TTC	TGG	CTC	ATC	TTC	AGC	ATC	4050
Asn	Val	Leu	Leu	Val	Cys	Leu	Ile	Phe	Trp	Leu	Ile	Phe	Ser	Ile	
				1340					1345					1350	
ATG	GGC	GTG	AAC	CTC	TTT	GCG	GGG	AAG	TTT	GGG	AGG	TGC	ATC	AAC	4095
Met	Gly	Val	Asn	Leu	Phe	Ala	Gly	Lys	Phe	Gly	Arg	Cys	Ile	Asn	
				1355					1360					1365	
CAG	ACA	GAG	GGA	GAC	TTG	CCT	TTG	AAC	TAC	ACC	ATC	GTG	AAC	AAC	4140
Gln	Thr	Glu	Gly	Asp	Leu	Pro	Leu	Asn	Tyr	Thr	Ile	Val	Asn	Asn	
				1370					1375					1380	
AAG	AGC	CAG	TGT	GAG	TCC	TTG	AAC	TTG	ACC	GGA	GAA	TTG	TAC	TGG	4185
Lys	Ser	Gln	Cys	Glu	Ser	Leu	Asn	Leu	Thr	Gly	Glu	Leu	Tyr	Trp	
				1385					1390					1395	
ACC	AAG	GTG	AAA	GTC	AAC	TTT	GAC	AAC	GTG	GGG	GCC	GGG	TAC	CTG	4230
Thr	Lys	Val	Lys	Val	Asn	Phe	Asp	Asn	Val	Gly	Ala	Gly	Tyr	Leu	
				1400					1405					1410	
GCC	CTT	CTG	CAG	GTG	GCA	ACA	TTT	AAA	GGC	TGG	ATG	GAC	ATT	ATG	4275

Ala	Leu	Leu	Gln	Val	Ala	Thr	Phe	Lys	Gly	Trp	Met	Asp	Ile	Met	
				1415					1420					1425	
TAT	GCA	GCT	GTG	GAC	TCC	AGG	GGG	TAT	GAA	GAG	CAG	CCT	CAG	TGG	4320
Tyr	Ala	Ala	Val	Asp	Ser	Arg	Gly	Tyr	Glu	Glu	Gln	Pro	Gln	Trp	
				1430					1435					1440	
GAA	TAC	AAC	CTC	TAC	ATG	TAC	ATC	TAT	TTT	GTC	ATT	TTC	ATC	ATC	4365
Glu	Tyr	Asn	Leu	Tyr	Met	Tyr	Ile	Tyr	Phe	Val	Ile	Phe	Ile	Ile	
				1445					1450					1455	
TTT	GGG	TCT	TTC	TTC	ACC	CTG	AAC	CTC	TTT	ATT	GGT	GTC	ATC	ATT	4410
Phe	Gly	Ser	Phe	Phe	Thr	Leu	Asn	Leu	Phe	Ile	Gly	Val	Ile	Ile	
				1460					1465					1470	
GAC	AAC	TTC	AAC	CAA	CAG	AAG	AAA	AAG	TTA	GGG	GGC	CAG	GAC	ATC	4455
Asp	Asn	Phe	Asn	Gln	Gln	Lys	Lys	Lys	Leu	Gly	Gly	Gln	Asp	Ile	
				1475					1480					1485	
TTC	ATG	ACA	GAG	GAG	CAG	AAG	AAG	TAC	TAC	AAT	GCC	ATG	AAG	AAG	4500
Phe	Met	Thr	Glu	Glu	Gln	Lys	Lys	Tyr	Tyr	Asn	Ala	Met	Lys	Lys	
				1490					1495					1500	
CTG	GGC	TCC	AAG	AAG	CCC	CAG	AAG	CCC	ATC	CCA	CGG	CCC	CTG	AAC	4545
Leu	Gly	Ser	Lys	Lys	Pro	Gln	Lys	Pro	Ile	Pro	Arg	Pro	Leu	Asn	
				1505					1510					1515	
AAG	TAC	CAG	GGC	TTC	ATA	TTC	GAC	ATT	GTG	ACC	AAG	CAG	GCC	TTT	4590
Lys	Tyr	Gln	Gly	Phe	Ile	Phe	Asp	Ile	Val	Thr	Lys	Gln	Ala	Phe	
				1520					1525					1530	
GAC	GTC	ACC	ATC	ATG	TTT	CTG	ATC	TGC	TTG	AAT	ATG	GTG	ACC	ATG	4635
Asp	Val	Thr	Ile	Met	Phe	Leu	Ile	Cys	Leu	Asn	Met	Val	Thr	Met	
				1535					1540					1545	
ATG	GTG	GAG	ACA	GAT	GAC	CAA	AGT	CCT	GAG	AAA	ATC	AAC	ATC	TTG	4680
Met	Val	Glu	Thr	Asp	Asp	Gln	Ser	Pro	Glu	Lys	Ile	Asn	Ile	Leu	
				1550					1555					1560	
GCC	AAG	ATC	AAC	CTG	CTC	TTT	GTG	GCC	ATC	TTC	ACA	GGC	GAG	TGT	4725
Ala	Lys	Ile	Asn	Leu	Leu	Phe	Val	Ala	Ile	Phe	Thr	Gly	Glu	Cys	
				1565					1570					1575	
ATT	GTC	AAG	CTG	GCT	GCC	CTG	CGC	CAC	TAC	TAC	TTC	ACC	AAC	AGC	4770
Ile	Val	Lys	Leu	Ala	Ala	Leu	Arg	His	Tyr	Tyr	Phe	Thr	Asn	Ser	
				1580					1585					1590	
TGG	AAT	ATC	TTC	GAC	TTC	GTG	GTT	GTC	ATC	CTC	TCC	ATC	GTG	GGC	4815
Trp	Asn	Ile	Phe	Asp	Phe	Val	Val	Val	Ile	Leu	Ser	Ile	Val	Gly	
				1595					1600					1605	
ACT	GTG	CTC	TCG	GAC	ATC	ATC	CAG	AAG	TAC	TTC	TTC	TCC	CCG	ACG	4860
Thr	Val	Leu	Ser	Asp	Ile	Ile	Gln	Lys	Tyr	Phe	Phe	Ser	Pro	Thr	
				1610					1615					1620	
CTC	TTC	CGA	GTC	ATC	CGC	CTG	GCC	CGA	ATA	GGC	CGC	ATC	CTC	AGA	4905
Leu	Phe	Arg	Val	Ile	Arg	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu	Arg	
				1625					1630					1635	
CTG	ATC	CGA	GGG	GCC	AAG	GGG	ATC	CGC	ACG	CTG	CTC	TTT	GCC	CTC	4950
Leu	Ile	Arg	Gly	Ala	Lys	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	

1640										1645					1650					
ATG	ATG	TCC	CTG	CCT	GCC	CTC	TTC	AAC	ATC	GGG	CTG	CTG	CTC	TTC	4995					
Met	Met	Ser	Leu	Pro	Ala	Leu	Phe	Asn	Ile	Gly	Leu	Leu	Leu	Phe						
				1655					1660					1665						
CTC	GTC	ATG	TTC	ATC	TAC	TCC	ATC	TTT	GGC	ATG	GCC	AAC	TTC	GCT	5040					
Leu	Val	Met	Phe	Ile	Tyr	Ser	Ile	Phe	Gly	Met	Ala	Asn	Phe	Ala						
				1670					1675					1680						
TAT	GTC	AAG	TGG	GAG	GCT	GGC	ATC	GAC	GAC	ATG	TTC	AAC	TTC	CAG	5085					
Tyr	Val	Lys	Trp	Glu	Ala	Gly	Ile	Asp	Asp	Met	Phe	Asn	Phe	Gln						
				1685					1690					1695						
ACC	TTC	GCC	AAC	AGC	ATG	CTG	TGC	CTC	TTC	CAG	ATC	ACC	ACG	TCG	5130					
Thr	Phe	Ala	Asn	Ser	Met	Leu	Cys	Leu	Phe	Gln	Ile	Thr	Thr	Ser						
				1700					1705					1710						
GCC	GGC	TGG	GAT	GGC	CTC	CTC	AGC	CCC	ATC	CTC	AAC	ACT	GGG	CCG	5175					
Ala	Gly	Trp	Asp	Gly	Leu	Leu	Ser	Pro	Ile	Leu	Asn	Thr	Gly	Pro						
				1715					1720					1725						
CCC	TAC	TGC	GAC	CCC	ACT	CTG	CCC	AAC	AGC	AAT	GGC	TCT	CGG	GGG	5220					
Pro	Tyr	Cys	Asp	Pro	Thr	Leu	Pro	Asn	Ser	Asn	Gly	Ser	Arg	Gly						
				1730					1735					1740						
GAC	TGC	GGG	AGC	CCA	GCC	GTG	GGC	ATC	CTC	TTC	TTC	ACC	ACC	TAC	5265					
Asp	Cys	Gly	Ser	Pro	Ala	Val	Gly	Ile	Leu	Phe	Phe	Thr	Thr	Tyr						
				1745					1750					1755						
ATC	ATC	ATC	TCC	TTC	CTC	ATC	GTG	GTC	AAC	ATG	TAC	ATT	GCC	ATC	5310					
Ile	Ile	Ile	Ser	Phe	Leu	Ile	Val	Val	Asn	Met	Tyr	Ile	Ala	Ile						
				1760					1765					1770						
ATC	CTG	GAG	AAC	TTC	AGC	GTG	GCC	ACG	GAG	GAG	AGC	ACC	GAG	CCC	5355					
Ile	Leu	Glu	Asn	Phe	Ser	Val	Ala	Thr	Glu	Glu	Ser	Thr	Glu	Pro						
				1775					1780					1785						
CTG	AGT	GAG	GAC	GAC	TTC	GAT	ATG	TTC	TAT	GAG	ATC	TGG	GAG	AAA	5400					
Leu	Ser	Glu	Asp	Asp	Phe	Asp	Met	Phe	Tyr	Glu	Ile	Trp	Glu	Lys						
				1790					1795					1800						
TTT	GAC	CCA	GAG	GCC	ACT	CAG	TTT	ATT	GAG	TAT	TCG	GTC	CTG	TCT	5445					
Phe	Asp	Pro	Glu	Ala	Thr	Gln	Phe	Ile	Glu	Tyr	Ser	Val	Leu	Ser						
				1805					1810					1815						
GAC	TTT	GCC	GAC	GCC	CTG	TCT	GAG	CCA	CTC	CGT	ATC	GCC	AAG	CCC	5490					
Asp	Phe	Ala	Asp	Ala	Leu	Ser	Glu	Pro	Leu	Ile	Arg	Ala	Lys	Pro						
				1820					1825					1830						
AAC	CAG	ATA	AGC	CTC	ATC	AAC	ATG	GAC	CTG	CCC	ATG	GTG	AGT	GGG	5535					
Asn	Gln	Ile	Ser	Leu	Ile	Asn	Met	Asp	Leu	Pro	Met	Val	Ser	Gly						
				1835					1840					1845						
GAC	CGC	ATC	CAT	TGC	ATG	GAC	ATT	CTC	TTT	GCC	TTC	ACC	AAA	AGG	5580					
Asp	Arg	Ile	His	Cys	Met	Asp	Ile	Leu	Phe	Ala	Phe	Thr	Lys	Arg						
				1850					1855					1860						
GTC	CTG	GGG	GAG	TCT	GGG	GAG	ATG	GAC	GCC	CTG	AAG	ATC	CAG	ATG	5625					
Val	Leu	Gly	Glu	Ser	Gly	Glu	Met	Asp	Ala	Leu	Lys	Ile	Gln	Met						
				1865					1870					1875						

GAG	GAG	AAG	TTC	ATG	GCA	GCC	AAC	CCA	TCC	AAG	ATC	TCC	TAC	GAG	5670
Glu	Glu	Lys	Phe	Met	Ala	Ala	Asn	Pro	Ser	Lys	Ile	Ser	Tyr	Glu	
				1880					1885					1890	
CCC	ATC	ACC	ACC	ACA	CTC	CGG	CGC	AAG	CAC	GAA	GAG	GTG	TCG	GCC	5715
Pro	Ile	Thr	Thr	Thr	Leu	Arg	Arg	Lys	His	Glu	Glu	Val	Ser	Ala	
				1895					1900					1905	
ATG	GTT	ATC	CAG	AGA	GCC	TTC	CGC	AGG	CAC	CTG	CTG	CAA	CGC	TCT	5760
Met	Val	Ile	Gln	Arg	Ala	Phe	Arg	Arg	His	Leu	Leu	Gln	Arg	Ser	
				1910					1915					1920	
TTG	AAG	CAT	GCC	TCC	TTC	CTC	TTC	CGT	CAG	CAG	GCG	GGC	AGC	GGC	5805
Leu	Lys	His	Ala	Ser	Phe	Leu	Phe	Arg	Gln	Gln	Ala	Gly	Ser	Gly	
				1925					1930					1935	
CTC	TCC	GAA	GAG	GAT	GCC	CCT	GAG	CGA	GAG	GGC	CTC	ATC	GCC	TAC	5850
Leu	Ser	Glu	Glu	Asp	Ala	Pro	Glu	Arg	Glu	Gly	Leu	Ile	Ala	Tyr	
				1940					1945					1950	
GTG	ATG	AGT	GAG	AAC	TTC	TCC	CGA	CCC	CTT	GGC	CCA	CCC	TCC	AGC	5895
Val	Met	Ser	Glu	Asn	Phe	Ser	Arg	Pro	Leu	Gly	Pro	Pro	Ser	Ser	
				1955					1960					1965	
TCC	TCC	ATC	TCC	TCC	ACT	TCC	TTC	CCA	CCC	TCC	TAT	GAC	AGT	GTC	5940
Ser	Ser	Ile	Ser	Ser	Thr	Ser	Phe	Pro	Pro	Ser	Tyr	Asp	Ser	Val	
				1970					1975					1980	
ACT	AGA	GCC	ACC	AGC	GAT	AAC	CTC	CAG	GTG	CGG	GGG	TCT	GAC	TAC	5985
Thr	Arg	Ala	Thr	Ser	Asp	Asn	Leu	Gln	Val	Arg	Gly	Ser	Asp	Tyr	
				1985					1990					1995	
AGC	CAC	AGT	GAA	GAT	CTC	GCC	GAC	TTC	CCC	CCT	TCT	CCG	GAC	AGG	6030
Ser	His	Ser	Glu	Asp	Leu	Ala	Asp	Phe	Pro	Pro	Ser	Pro	Asp	Arg	
				2000					2005					2010	
GAC	CGT	GAG	TCC	ATC	GTG										6048
Asp	Arg	Glu	Ser	Ile	Val										
				2015											

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2016 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Asn	Phe	Leu	Leu	Pro	Arg	Gly	Thr	Ser	Ser	Phe	Arg	Arg	
1				5					10					15	
Phe	Thr	Arg	Glu	Ser	Leu	Ala	Ala	Ile	Glu	Lys	Arg	Met	Ala	Glu	
				20					25					30	
Lys	Gln	Ala	Arg	Gly	Ser	Thr	Thr	Leu	Gln	Glu	Ser	Arg	Glu	Gly	
				35					40					45	
Leu	Pro	Glu	Glu	Glu	Ala	Pro	Arg	Pro	Gln	Leu	Asp	Leu	Gln	Ala	
				50					55					60	

Ser	Lys	Lys	Leu	Pro	Asp	Leu	Tyr	Gly	Asn	Pro	Pro	Gln	Glu	Leu	65	70	75
Ile	Gly	Glu	Pro	Leu	Glu	Asp	Leu	Asp	Pro	Phe	Tyr	Ser	Thr	Gln	80	85	90
Lys	Thr	Phe	Ile	Val	Leu	Asn	Lys	Gly	Lys	Thr	Ile	Phe	Arg	Phe	95	100	105
Ser	Ala	Thr	Asn	Ala	Leu	Tyr	Val	Leu	Ser	Pro	Phe	His	Pro	Val	110	115	120
Arg	Arg	Ala	Ala	Val	Lys	Ile	Leu	Val	His	Ser	Leu	Phe	Asn	Met	125	130	135
Leu	Ile	Met	Cys	Thr	Ile	Leu	Thr	Asn	Cys	Val	Phe	Met	Ala	Gln	140	145	150
His	Asp	Pro	Pro	Pro	Trp	Thr	Lys	Tyr	Val	Glu	Tyr	Thr	Phe	Thr	155	160	165
Ala	Ile	Tyr	Thr	Phe	Glu	Ser	Leu	Val	Lys	Ile	Leu	Ala	Arg	Ala	170	175	180
Phe	Cys	Leu	His	Ala	Phe	Thr	Phe	Leu	Arg	Asp	Pro	Trp	Asn	Trp	185	190	195
Leu	Asp	Phe	Ser	Val	Ile	Ile	Met	Ala	Tyr	Thr	Thr	Glu	Phe	Val	200	205	210
Asp	Leu	Gly	Asn	Val	Ser	Ala	Leu	Arg	Thr	Phe	Arg	Val	Leu	Arg	215	220	225
Ala	Leu	Lys	Thr	Ile	Ser	Val	Ile	Ser	Gly	Leu	Lys	Thr	Ile	Val	230	235	240
Gly	Ala	Leu	Ile	Gln	Ser	Val	Lys	Lys	Leu	Ala	Asp	Val	Met	Val	245	250	255
Leu	Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Ile	Gly	Leu	Gln	260	265	270
Leu	Phe	Met	Gly	Asn	Leu	Arg	His	Lys	Cys	Val	Arg	Asn	Phe	Thr	275	280	285
Ala	Leu	Asn	Gly	Thr	Asn	Gly	Ser	Val	Glu	Ala	Asp	Gly	Leu	Val	290	295	300
Trp	Glu	Ser	Leu	Asp	Leu	Tyr	Leu	Ser	Asp	Pro	Glu	Asn	Tyr	Leu	305	310	315
Leu	Lys	Asn	Gly	Thr	Ser	Asp	Val	Leu	Leu	Cys	Gly	Asn	Ser	Ser	320	325	330
Asp	Ala	Gly	Thr	Cys	Pro	Glu	Gly	Tyr	Arg	Cys	Leu	Lys	Ala	Gly	335	340	345
Glu	Asn	Pro	Asp	His	Gly	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Ala	Trp	350	355	360
Ala	Phe	Leu	Ala	Leu	Phe	Arg	Leu	Met	Thr	Gln	Asp	Cys	Trp	Glu	365	370	375

Arg	Leu	Tyr	Gln	Gln	Thr	Leu	Arg	Ser	Ala	Gly	Lys	Ile	Tyr	Met	380	385	390
Ile	Phe	Phe	Met	Leu	Val	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	395	400	405
Asn	Leu	Ile	Leu	Ala	Val	Val	Ala	Met	Ala	Tyr	Glu	Glu	Gln	Asn	410	415	420
Gln	Ala	Thr	Ile	Ala	Glu	Thr	Glu	Glu	Lys	Glu	Lys	Arg	Phe	Gln	425	430	435
Glu	Ala	Met	Glu	Met	Leu	Lys	Lys	Glu	His	Glu	Ala	Leu	Thr	Ile	440	445	450
Arg	Gly	Val	Asp	Thr	Val	Ser	Arg	Ser	Ser	Leu	Glu	Met	Ser	Pro	455	460	465
Leu	Ala	Pro	Val	Asn	Ser	His	Glu	Arg	Arg	Ser	Lys	Arg	Arg	Lys	470	475	480
Arg	Met	Ser	Ser	Gly	Thr	Glu	Glu	Cys	Gly	Glu	Asp	Arg	Leu	Pro	485	490	495
Lys	Ser	Asp	Ser	Glu	Asp	Gly	Pro	Arg	Ala	Met	Asn	His	Leu	Ser	500	505	510
Leu	Thr	Arg	Gly	Leu	Ser	Arg	Thr	Ser	Met	Lys	Pro	Arg	Ser	Ser	515	520	525
Arg	Gly	Ser	Ile	Phe	Thr	Phe	Arg	Arg	Arg	Asp	Leu	Gly	Ser	Glu	530	535	540
Ala	Asp	Phe	Ala	Asp	Asp	Glu	Asn	Ser	Thr	Ala	Arg	Glu	Ser	Glu	545	550	555
Ser	His	His	Thr	Ser	Leu	Leu	Val	Pro	Trp	Pro	Leu	Arg	Arg	Thr	560	565	570
Ser	Ala	Gln	Gly	Gln	Pro	Ser	Pro	Gly	Thr	Ser	Ala	Pro	Gly	His	575	580	585
Ala	Leu	His	Gly	Lys	Lys	Asn	Ser	Thr	Val	Asp	Cys	Asn	Gly	Val	590	595	600
Val	Ser	Leu	Leu	Gly	Ala	Gly	Asp	Pro	Glu	Ala	Thr	Ser	Pro	Gly	605	610	615
Ser	His	Leu	Leu	Arg	Pro	Val	Met	Leu	Glu	His	Pro	Pro	Asp	Thr	620	625	630
Thr	Thr	Pro	Ser	Glu	Glu	Pro	Gly	Gly	Pro	Gln	Met	Leu	Thr	Ser	635	640	645
Gln	Ala	Pro	Cys	Val	Asp	Gly	Phe	Glu	Glu	Pro	Gly	Ala	Arg	Gln	650	655	660
Arg	Ala	Leu	Ser	Ala	Val	Ser	Val	Leu	Thr	Ser	Ala	Leu	Glu	Glu	665	670	675

Leu	Glu	Glu	Ser	Arg	His	Lys	Cys	Pro	Pro	Cys	Trp	Asn	Arg	Leu	680	685	690
Ala	Gln	Arg	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	Leu	Trp	Met	Ser	695	700	705
Ile	Lys	Gln	Gly	Val	Lys	Leu	Val	Val	Met	Asp	Pro	Phe	Thr	Asp	710	715	720
Leu	Thr	Ile	Thr	Met	Cys	Ile	Val	Leu	Asn	Thr	Leu	Phe	Met	Ala	725	730	735
Leu	Glu	His	Tyr	Asn	Met	Thr	Ser	Glu	Phe	Glu	Glu	Met	Leu	Gln	740	745	750
Val	Gly	Asn	Leu	Val	Phe	Thr	Gly	Ile	Phe	Thr	Ala	Glu	Met	Thr	755	760	765
Phe	Lys	Ile	Ile	Ala	Leu	Asp	Pro	Tyr	Tyr	Tyr	Phe	Gln	Gln	Gly	770	775	780
Trp	Asn	Ile	Phe	Asp	Ser	Ile	Ile	Val	Ile	Leu	Ser	Leu	Met	Glu	785	790	795
Leu	Gly	Leu	Ser	Arg	Met	Ser	Asn	Leu	Ser	Val	Leu	Arg	Ser	Phe	800	805	810
Arg	Leu	Leu	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	815	820	825
Asn	Thr	Leu	Ile	Lys	Ile	Ile	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	830	835	840
Asn	Leu	Thr	Leu	Val	Leu	Ala	Ile	Ile	Val	Phe	Ile	Phe	Ala	Val	845	850	855
Val	Gly	Met	Gln	Leu	Phe	Gly	Lys	Asn	Tyr	Ser	Glu	Leu	Arg	Asp	860	865	870
Ser	Asp	Ser	Gly	Leu	Leu	Pro	Arg	Trp	His	Met	Met	Asp	Phe	Phe	875	880	885
His	Ala	Phe	Leu	Ile	Ile	Phe	Arg	Ile	Leu	Cys	Gly	Glu	Trp	Ile	890	895	900
Glu	Thr	Met	Trp	Asp	Cys	Met	Glu	Val	Ser	Gly	Gln	Ser	Leu	Cys	905	910	915
Leu	Leu	Val	Phe	Leu	Leu	Val	Met	Val	Ile	Gly	Asn	Leu	Val	Val	920	925	930
Leu	Asn	Leu	Phe	Leu	Ala	Leu	Leu	Leu	Ser	Ser	Phe	Ser	Ala	Asp	935	940	945
Asn	Leu	Thr	Ala	Pro	Asp	Glu	Asp	Arg	Glu	Met	Asn	Asn	Leu	Gln	950	955	960
Leu	Ala	Leu	Ala	Arg	Ile	Gln	Arg	Gly	Leu	Arg	Phe	Val	Lys	Arg	965	970	975
Thr	Thr	Trp	Asp	Phe	Cys	Cys	Gly	Leu	Leu	Arg	His	Arg	Pro	Gln			

980					985					990				
Lys	Pro	Ala	Ala	Leu	Ala	Ala	Gln	Gly	Gln	Leu	Pro	Ser	Cys	Ile
				995					1000					1005
Ala	Thr	Pro	Tyr	Ser	Pro	Pro	Pro	Pro	Glu	Thr	Glu	Lys	Val	Pro
				1010					1015					1020
Pro	Thr	Arg	Lys	Glu	Thr	Gln	Phe	Glu	Glu	Gly	Glu	Gln	Pro	Gly
				1025					1030					1035
Gln	Gly	Thr	Pro	Gly	Asp	Pro	Glu	Pro	Val	Cys	Val	Pro	Ile	Ala
				1040					1045					1050
Val	Ala	Glu	Ser	Asp	Thr	Asp	Asp	Gln	Glu	Glu	Asp	Glu	Glu	Asn
				1055					1060					1065
Ser	Leu	Gly	Thr	Glu	Glu	Glu	Ser	Ser	Lys	Gln	Gln	Glu	Ser	Gln
				1070					1075					1080
Pro	Val	Ser	Gly	Trp	Pro	Arg	Gly	Pro	Pro	Asp	Ser	Arg	Thr	Trp
				1085					1090					1095
Ser	Gln	Val	Ser	Ala	Thr	Ala	Ser	Ser	Glu	Ala	Glu	Ala	Ser	Ala
				1100					1105					1110
Ser	Gln	Ala	Asp	Trp	Arg	Gln	Gln	Trp	Lys	Ala	Glu	Pro	Gln	Ala
				1115					1120					1125
Pro	Gly	Cys	Gly	Glu	Thr	Pro	Glu	Asp	Ser	Cys	Ser	Glu	Gly	Ser
				1130					1135					1140
Thr	Ala	Asp	Met	Thr	Asn	Thr	Ala	Glu	Leu	Leu	Glu	Gln	Ile	Pro
				1145					1150					1155
Asp	Leu	Gly	Gln	Asp	Val	Lys	Asp	Pro	Glu	Asp	Cys	Phe	Thr	Glu
				1160					1165					1170
Gly	Cys	Val	Arg	Arg	Cys	Pro	Cys	Cys	Ala	Val	Asp	Thr	Thr	Gln
				1175					1180					1185
Ala	Pro	Gly	Lys	Val	Trp	Trp	Arg	Leu	Arg	Lys	Thr	Cys	Tyr	His
				1190					1195					1200
Ile	Val	Glu	His	Ser	Trp	Phe	Glu	Thr	Phe	Ile	Ile	Phe	Met	Ile
				1205					1210					1215
Leu	Leu	Ser	Ser	Gly	Ala	Leu	Ala	Phe	Glu	Asp	Ile	Tyr	Leu	Glu
				1220					1225					1230
Glu	Arg	Lys	Thr	Ile	Lys	Val	Leu	Leu	Glu	Tyr	Ala	Asp	Lys	Met
				1235					1240					1245
Phe	Thr	Tyr	Val	Phe	Val	Leu	Glu	Met	Leu	Leu	Lys	Trp	Val	Ala
				1250					1255					1260
Tyr	Gly	Phe	Lys	Lys	Tyr	Phe	Thr	Asn	Ala	Trp	Cys	Trp	Leu	Asp
				1265					1270					1275
Phe	Leu	Ile	Val	Asp	Val	Ser	Leu	Val	Ser	Leu	Val	Ala	Asn	Thr
				1280					1285					1290

Leu Gly Phe Ala	Glu Met Gly Pro Ile	Lys Ser Leu Arg Thr	Leu
	1295	1300	1305
Arg Ala Leu Arg	Pro Leu Arg Ala Leu	Ser Arg Phe Glu Gly	Met
	1310	1315	1320
Arg Val Val Val	Asn Ala Leu Val Gly	Ala Ile Pro Ser Ile	Met
	1325	1330	1335
Asn Val Leu Leu	Val Cys Leu Ile Phe	Trp Leu Ile Phe Ser	Ile
	1340	1345	1350
Met Gly Val Asn	Leu Phe Ala Gly Lys	Phe Gly Arg Cys Ile	Asn
	1355	1360	1365
Gln Thr Glu Gly	Asp Leu Pro Leu Asn	Tyr Thr Ile Val Asn	Asn
	1370	1375	1380
Lys Ser Gln Cys	Glu Ser Leu Asn Leu	Thr Gly Glu Leu Tyr	Trp
	1385	1390	1395
Thr Lys Val Lys	Val Asn Phe Asp Asn	Val Gly Ala Gly Tyr	Leu
	1400	1405	1410
Ala Leu Leu Gln	Val Ala Thr Phe Lys	Gly Trp Met Asp Ile	Met
	1415	1420	1425
Tyr Ala Ala Val	Asp Ser Arg Gly Tyr	Glu Glu Gln Pro Gln	Trp
	1430	1435	1440
Glu Tyr Asn Leu	Tyr Met Tyr Ile Tyr	Phe Val Ile Phe Ile	Ile
	1445	1450	1455
Phe Gly Ser Phe	Phe Thr Leu Asn Leu	Phe Ile Gly Val Ile	Ile
	1460	1465	1470
Asp Asn Phe Asn	Gln Gln Lys Lys Lys	Leu Gly Gly Gln Asp	Ile
	1475	1480	1485
Phe Met Thr Glu	Glu Gln Lys Lys Tyr	Tyr Asn Ala Met Lys	Lys
	1490	1495	1500
Leu Gly Ser Lys	Lys Pro Gln Lys Pro	Ile Pro Arg Pro Leu	Asn
	1505	1510	1515
Lys Tyr Gln Gly	Phe Ile Phe Asp Ile	Val Thr Lys Gln Ala	Phe
	1520	1525	1530
Asp Val Thr Ile	Met Phe Leu Ile Cys	Leu Asn Met Val Thr	Met
	1535	1540	1545
Met Val Glu Thr	Asp Asp Gln Ser Pro	Glu Lys Ile Asn Ile	Leu
	1550	1555	1560
Ala Lys Ile Asn	Leu Leu Phe Val Ala	Ile Phe Thr Gly Glu	Cys
	1565	1570	1575
Ile Val Lys Leu	Ala Ala Leu Arg His	Tyr Tyr Phe Thr Asn	Ser
	1580	1585	1590

Trp	Asn	Ile	Phe	Asp	Phe	Val	Val	Val	Ile	Leu	Ser	Ile	Val	Gly	
				1595					1600					1605	
Thr	Val	Leu	Ser	Asp	Ile	Ile	Gln	Lys	Tyr	Phe	Phe	Ser	Pro	Thr	
				1610					1615					1620	
Leu	Phe	Arg	Val	Ile	Arg	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu	Arg	
				1625					1630					1635	
Leu	Ile	Arg	Gly	Ala	Lys	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	
				1640					1645					1650	
Met	Met	Ser	Leu	Pro	Ala	Leu	Phe	Asn	Ile	Gly	Leu	Leu	Leu	Phe	
				1655					1660					1665	
Leu	Val	Met	Phe	Ile	Tyr	Ser	Ile	Phe	Gly	Met	Ala	Asn	Phe	Ala	
				1670					1675					1680	
Tyr	Val	Lys	Trp	Glu	Ala	Gly	Ile	Asp	Asp	Met	Phe	Asn	Phe	Gln	
				1685					1690					1695	
Thr	Phe	Ala	Asn	Ser	Met	Leu	Cys	Leu	Phe	Gln	Ile	Thr	Thr	Ser	
				1700					1705					1710	
Ala	Gly	Trp	Asp	Gly	Leu	Leu	Ser	Pro	Ile	Leu	Asn	Thr	Gly	Pro	
				1715					1720					1725	
Pro	Tyr	Cys	Asp	Pro	Thr	Leu	Pro	Asn	Ser	Asn	Gly	Ser	Arg	Gly	
				1730					1735					1740	
Asp	Cys	Gly	Ser	Pro	Ala	Val	Gly	Ile	Leu	Phe	Phe	Thr	Thr	Tyr	
				1745					1750					1755	
Ile	Ile	Ile	Ser	Phe	Leu	Ile	Val	Val	Asn	Met	Tyr	Ile	Ala	Ile	
				1760					1765					1770	
Ile	Leu	Glu	Asn	Phe	Ser	Val	Ala	Thr	Glu	Glu	Ser	Thr	Glu	Pro	
				1775					1780					1785	
Leu	Ser	Glu	Asp	Asp	Phe	Asp	Met	Phe	Tyr	Glu	Ile	Trp	Glu	Lys	
				1790					1795					1800	
Phe	Asp	Pro	Glu	Ala	Thr	Gln	Phe	Ile	Glu	Tyr	Ser	Val	Leu	Ser	
				1805					1810					1815	
Asp	Phe	Ala	Asp	Ala	Leu	Ser	Glu	Pro	Leu	Ile	Arg	Ala	Lys	Pro	
				1820					1825					1830	
Asn	Gln	Ile	Ser	Leu	Ile	Asn	Met	Asp	Leu	Pro	Met	Val	Ser	Gly	
				1835					1840					1845	
Asp	Arg	Ile	His	Cys	Met	Asp	Ile	Leu	Phe	Ala	Phe	Thr	Lys	Arg	
				1850					1855					1860	
Val	Leu	Gly	Glu	Ser	Gly	Glu	Met	Asp	Ala	Leu	Lys	Ile	Gln	Met	
				1865					1870					1875	
Glu	Glu	Lys	Phe	Met	Ala	Ala	Asn	Pro	Ser	Lys	Ile	Ser	Tyr	Glu	
				1880					1885					1890	
Pro	Ile	Thr	Thr	Thr	Leu	Arg	Arg	Lys	His	Glu	Glu	Val	Ser	Ala	

1895					1900					1905				
Met	Val	Ile	Gln	Arg	Ala	Phe	Arg	Arg	His	Leu	Leu	Gln	Arg	Ser
				1910										1920
Leu	Lys	His	Ala	Ser	Phe	Leu	Phe	Arg	Gln	Gln	Ala	Gly	Ser	Gly
				1925										1935
Leu	Ser	Glu	Glu	Asp	Ala	Pro	Glu	Arg	Glu	Gly	Leu	Ile	Ala	Tyr
				1940										1950
Val	Met	Ser	Glu	Asn	Phe	Ser	Arg	Pro	Leu	Gly	Pro	Pro	Ser	Ser
				1955										1965
Ser	Ser	Ile	Ser	Ser	Thr	Ser	Phe	Pro	Pro	Ser	Tyr	Asp	Ser	Val
				1970										1980
Thr	Arg	Ala	Thr	Ser	Asp	Asn	Leu	Gln	Val	Arg	Gly	Ser	Asp	Tyr
				1985										1995
Ser	His	Ser	Glu	Asp	Leu	Ala	Asp	Phe	Pro	Pro	Ser	Pro	Asp	Arg
				2000										2010
Asp	Arg	Glu	Ser	Ile	Val									
				2015										

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCAAAC TCCTATTACC TCGG 24

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CACGATGGAC TCACGGTCCC TGTC 24

- (2) INFORMATION FOR SEQ ID NO:5:
- (I) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3069 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG	GGG	AAG	GGG	GTT	GGA	CGT	GAT	AAG	TAT	GAG	CCT	GCA	GCT	GTT	45
Met	Gly	Lys	Gly	Val	Gly	Arg	Asp	Lys	Tyr	Glu	Pro	Ala	Ala	Val	
1				5					10					15	

TCA GAA CAA GGT GAT AAA AAG GGC AAA AAG GGC AAA AAA GAC AGG	90
Ser Glu Gln Glu Asp Lys Lys Glu Lys Lys Glu Lys Lys Asp Arg	
20 25 30	
GAC ATG GAT GAA CTG AAG AAA GAA GTT TCT ATG GAT GAT CAT AAA	135
Asp Met Asp Glu Leu Lys Lys Glu Val Ser Met Asp Asp His Lys	
35 40 45	
CTT AGC CTT GAT GAA CTT CAT CGT AAA TAT GGA ACA GAC TTG AGC	180
Leu Ser Leu Asp Glu Leu His Arg Lys Tyr Gly Thr Asp Leu Ser	
50 55 60	
CGG GGA TTA ACA TCT GCT CGT GCA GCT GAG ATC CTG GCG CGA GAT	225
Arg Gly Leu Thr Ser Ala Arg Ala Ala Glu Ile Leu Ala Arg Asp	
65 70 75	
GGT CCC AAC GCC CTC ACT CCC CCT CCC ACT ACT CCT GAA TGG ATC	270
Gly Pro Asn Ala Leu Thr Pro Pro Pro Thr Thr Pro Glu Trp Ile	
80 85 90	
AAG TTT TGT CGG CAG CTC TTT GGG GGG TTC TCA ATG TTA CTG TGG	315
Lys Phe Cys Arg Gln Leu Phe Gly Gly Phe Ser Met Leu Leu Trp	
95 100 105	
ATT GGA GCG ATT CTT TGT TTC TTG GCT TAT AGC ATC CAA GCT GCT	360
Ile Gly Ala Ile Leu Cys Phe Leu Ala Tyr Ser Ile Gln Ala Ala	
110 115 120	
ACA GAA GAG GAA CCT CAA AAC GAT AAT CTG TAC CTG GGT GTG GTG	405
Thr Glu Glu Glu Pro Gln Asn Asp Asn Leu Tyr Leu Gly Val Val	
125 130 135	
CTA TCA GCC GTT GTA ATC ATA ACT GGT TGC TTC TCC TAC TAT CAA	450
Leu Ser Ala Val Val Ile Ile Thr Gly Cys Phe Ser Tyr Tyr Gln	
140 145 150	
GAA GCT AAA AGT TCA AAG ATC ATG GAA TCC TTC AAA AAC ATG GTC	495
Glu Ala Lys Ser Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val	
155 160 165	
CCT CAG CAA GCC CTT GTG ATT CGA AAT GGT GAG AAA ATG AGC ATA	540
Pro Gln Gln Ala Leu Val Ile Arg Asn Gly Glu Lys Met Ser Ile	
170 175 180	
AAT GCG GAG GAA GTT GTG GTT GGG GAT CTG GTG GAA GTA AAA GGA	585
Asn Ala Glu Glu Val Val Val Gly Asp Lue Val Glu Val Lys Gly	
185 190 195	
GGA GAC CGA ATT CCT GCT GAC CTC AGA ATC ATA TCT GCA AAT GGC	630
Gly Asp Arg Ile Pro Ala Asp Leu Arg Ile Ile Ser Ala Asn Gly	
200 205 210	
TGC AAG GTG GAT AAC TCC TCG CTC ACT GGT GAA TCA GAA CCC CAG	675
Cys Lys Val Asp Asn Ser Ser Leu Thr Gly Glu Ser Glu Pro Gln	
215 220 225	
ACT AGG TCT CCA GAT TTC ACA AAT GAA AAC CCC CTG GAG ACG AGG	720
Thr Arg Ser Pro Asp Phe Thr Asn Glu Asn Pro Leu Glu Thr Arg	
230 235 240	
AAC ATT GCC TTC TTT TCA ACA AAT TGT GTT GAA GGC ACC GCA CGT	765
Asn Ile Ala Phe Phe Ser Thr Asn Cys Val Glu Gly Thr Ala Arg	

				245					250					255	
GGT	ATT	GTT	GTC	TAC	ACT	GGG	GAT	CGC	ACT	GTG	ATG	GGA	AGA	ATT	810
Gly	Ile	Val	Val	Tyr	Thr	Gly	Asp	Arg	Thr	Val	Met	Gly	Arg	Ile	
				260					265					270	
GCC	ACA	CTT	GCT	TCT	GGG	CTG	GAA	GGA	GGC	CAG	ACC	CCC	ATT	GCT	855
Ala	Thr	Leu	Ala	Ser	Gly	Leu	Glu	Gly	Gly	Gln	Thr	Pro	Ile	Ala	
				275					280					285	
GCA	GAA	ATT	GAA	CAT	TTT	ATC	CAC	ATC	ATC	ACG	GGT	GTG	GCT	GTG	900
Ala	Glu	Ile	Glu	His	Phe	Ile	His	Ile	Ile	Thr	Gly	Val	Ala	Val	
				290					295					300	
TTC	CTG	GGT	GTG	TCT	TTC	TTC	ATC	CTT	TCT	CTC	ATC	CTT	GAG	TAC	945
Phe	Leu	Gly	Val	Ser	Phe	Phe	Ile	Leu	Ser	Leu	Ile	Leu	Glu	Tyr	
				305					310					315	
ACC	TGG	CTT	GAG	GCT	GTC	ATC	TTC	CTC	ATC	GGT	ATC	ATC	GTA	GCC	990
Thr	Trp	Leu	Glu	Ala	Val	Ile	Phe	Leu	Ile	Gly	Ile	Ile	Val	Ala	
				320					325					330	
AAT	GTG	CCG	GAA	GGT	TTG	CTG	GCC	ACT	GTC	ACG	GTC	TGT	CTG	ACA	1035
Asn	Val	Pro	Glu	Gly	Leu	Leu	Ala	Thr	Val	Thr	Val	Cys	Leu	Thr	
				335					340					345	
CTT	ACT	GCC	AAA	CGC	ATG	GCA	AGG	AAA	AAC	TGC	TTA	GTG	AAG	AAC	1080
Leu	Thr	Ala	Lys	Arg	Met	Ala	Arg	Lys	Asn	Cys	Leu	Val	Lys	Asn	
				350					355					360	
TTA	GAA	GCT	GTG	GAG	ACC	TTG	GGG	TCC	ACG	TCC	ACC	ATC	TGC	TCT	1125
Leu	Glu	Ala	Val	Glu	Thr	Leu	Gly	Ser	Thr	Ser	Thr	Ile	Cys	Ser	
				365					370					375	
GAT	AAA	ACT	GGA	ACT	CTG	ACT	CAG	AAC	CGG	ATG	ACA	GTG	GCC	CAC	1170
Asp	Lys	Thr	Gly	Thr	Leu	Thr	Gln	Asn	Arg	Met	Thr	Val	Ala	His	
				380					385					390	
ATG	TGG	TTT	GAC	AAT	CAA	ATC	CAT	GAA	GCT	GAT	ACG	ACA	GAG	AAT	1215
Met	Trp	Phe	Asp	Asn	Gln	Ile	His	Glu	Ala	Asp	Thr	Thr	Glu	Asn	
				395					400					405	
CAG	AGT	GGT	GTC	TCT	TTT	GAC	AAG	ACT	TCA	GCT	ACC	TGG	CTT	GCT	1260
Gln	Ser	Gly	Val	Ser	Phe	Asp	Lys	Thr	Ser	Ala	Thr	Trp	Leu	Ala	
				410					415					420	
CTG	TCC	AGA	ATT	GCA	GGT	CTT	TGT	AAC	AGG	GCA	GTG	TTT	CAG	GCT	1305
Leu	Ser	Arg	Ile	Ala	Gly	Leu	Cys	Asn	Arg	Ala	Val	Phe	Gln	Ala	
				425					430					435	
AAC	CAG	GAA	AAC	CTA	CCT	ATT	CTT	AAG	CGG	GCA	GTT	GCA	GGA	GAT	1350
Asn	Gln	Glu	Asn	Leu	Pro	Ile	Leu	Lys	Arg	Ala	Val	Ala	Gly	Asp	
				440					445					450	
GCC	TCT	GAG	TCA	GCA	CTC	TTA	AAG	TGC	ATA	GAG	CTG	TGC	TGT	GGT	1395
Ala	Ser	Glu	Ser	Ala	Leu	Leu	Lys	Cys	Ile	Glu	Leu	Cys	Cys	Gly	
				455					460					465	
TTC	GTG	AAG	GAG	ATG	AGA	GAA	AGA	TAC	GCC	AAA	ATC	GTC	GAG	ATA	1440
Ser	Val	Lys	Glu	Met	Arg	Glu	Arg	Tyr	Ala	Lys	Ile	Val	Glu	Ile	
				470					475					480	

CCC	TTC	AAC	TCC	ACC	AAC	AAG	TAC	CAG	TTG	TCT	ATT	CAT	AAG	AAC	1485
Pro	Phe	Asn	Ser	Thr	Asn	Lys	Tyr	Gln	Leu	Ser	Ile	His	Lys	Asn	
				485					490					495	
CCC	AAC	ACA	TCG	GAG	CCC	CAA	CAC	CTG	TTG	GTG	ATG	AAG	GGC	GCC	1520
Pro	Asn	Thr	Ser	Glu	Pro	Gln	His	Leu	Leu	Val	Met	Lys	Gly	Ala	
				500					505					510	
CCA	GAA	AGG	ATC	CTA	GAC	CGT	TGC	AGC	TCT	ATC	CTC	CTC	CAC	GGC	1565
Pro	Glu	Arg	Ile	Leu	Asp	Arg	Cys	Ser	Ser	Ile	Leu	Leu	His	Gly	
				515					520					525	
AAG	GAG	CAG	CCC	CTG	GAT	GAG	GAG	CTG	AAA	GAC	GCC	TTT	CAG	AAC	1620
Lys	Glu	Gln	Pro	Leu	Asp	Glu	Glu	Leu	Lys	Asp	Ala	Phe	Gln	Asn	
				530					535					540	
GCC	TAT	TTG	GAG	CTG	GGG	GGC	CTC	GGA	GAA	CGA	GTC	CTA	GGT	TTC	1665
Ala	Tyr	Leu	Glu	Leu	Gly	Gly	Leu	Gly	Glu	Arg	Val	Leu	Gly	Phe	
				545					550					555	
TGC	CAC	CTC	TTT	CTG	CCA	GAT	GAA	CAG	TTT	CCT	GAA	GGG	TTC	CAG	1710
Cys	His	Leu	Phe	Leu	Pro	Asp	Glu	Gln	Phe	Pro	Glu	Gly	Phe	Gln	
				560					565					570	
TTT	GAC	ACT	GAC	GAT	GTG	AAT	TTC	CCT	ATC	GAT	AAT	CTG	TGC	TTC	1755
Phe	Asp	Thr	Asp	Asp	Val	Asn	Phe	Pro	Ile	Asp	Asn	Leu	Cys	Phe	
				575					580					585	
GTT	GGG	CTC	ATC	TCC	ATG	ATT	GAC	CCT	CCA	CGG	GCG	GCC	GTT	CCT	1800
Val	Gly	Leu	Ile	Ser	Met	Ile	Asp	Pro	Pro	Arg	Ala	Ala	Val	Pro	
				590					595					600	
GAT	GCC	GTG	GGC	AAA	TGT	CGA	AGT	GCT	GGA	ATT	AAG	GTC	ATC	ATG	1845
Asp	Ala	Val	Gly	Lys	Cys	Arg	Ser	Aal	Gly	Ile	Lys	Val	Ile	Met	
				605					610					615	
GTC	ACA	GGA	GAC	CAT	CCA	ATC	ACA	GCT	AAA	GCT	ATT	GCC	AAA	GGT	1890
Val	Thr	Gly	Asp	His	Pro	Ile	Thr	Ala	Lys	Ala	Ile	Ala	Lys	Gly	
				620					625					630	
GTG	GGC	ATC	ATC	TCA	GAA	GGC	ATG	GAG	ACC	GTG	GAA	GAC	ATT	GCT	1935
Val	Gly	Ile	Ile	Ser	Glu	Gly	Asn	Glu	Thr	Val	Glu	Asp	Ile	Ala	
				635					640					645	
GCC	CGC	CTC	AAC	ATC	CCA	GTC	AGC	CAG	GTG	AAC	CCC	AGG	GAT	GCC	1980
Ala	Arg	Leu	Asn	Ile	Pro	Val	Ser	Gln	Val	Asn	Pro	Arg	Asp	Ala	
				650					655					660	
AAG	GCC	TGC	GTA	GTA	CAC	GGC	AGT	GAT	CTA	AAG	GAC	ATG	ACC	TCC	2025
Lys	Ala	Cys	Val	Val	His	Gly	Ser	Asp	Leu	Lys	Asp	Met	Thr	Ser	
				665					670					675	
GAG	CAG	CTG	GAT	GAC	ATT	TTG	AAG	TAC	CAC	ACT	GAG	ATA	GTG	TTT	2070
Glu	Glm	Leu	Asp	Asp	Ile	Leu	Lys	Tyr	His	Thr	Glu	Ile	Val	Phe	
				680					685					690	
GCC	AGG	ACC	TCC	CCT	CAG	CAG	AAG	CTC	ATC	ATT	GTG	GAA	GGC	TGC	2115
Ala	Arg	Thr	Ser	Pro	Gln	Gln	Lys	Leu	Ile	Ile	Val	Glu	Gly	Cys	
				695					700					705	

CAA	AGA	CAG	GGT	GCT	ATC	GTG	GCT	GTG	ACT	GGT	GAC	GGT	GTG	AAT	2160
Gln	Arg	Gln	Gly	Ala	Ile	Val	Ala	Val	Thr	Gly	Asp	Gly	Val	Asn	
				710					715					720	
GAC	TCT	CCA	GCT	TTG	AAG	AAA	GCA	GAC	ATT	GGG	GTT	GCT	ATG	GGG	2205
Asp	Ser	Pro	Ala	Leu	Lys	Lys	Ala	Asp	Ile	Gly	Val	Ala	Met	Gly	
				725					730					735	
ATT	GCT	GGC	TCA	GAT	GTG	TCC	AAG	CAA	GCT	GCT	GAC	ATG	ATT	CTT	2250
Ile	Ala	Gly	Ser	Asp	Val	Ser	Lys	Gln	Ala	Ala	Asp	Met	Ile	Leu	
				740					745					750	
CTG	GAT	GAC	AAC	TTT	GCC	TCA	ATT	GTG	ACT	GGA	GTA	GAG	GAA	GGT	2295
Leu	Asp	Asp	Asn	Phe	Ala	Ser	Ile	Val	Thr	Gly	Val	Glu	Glu	Gly	
				755					760					765	
CGT	CTG	ATC	TTT	GAT	AAC	TTG	AAG	AAA	TCC	ATT	GCT	TAT	ACC	TTA	2340
Arg	Leu	Ile	Phe	Asp	Asn	Leu	Lys	Lys	Ser	Ile	Ala	Tyr	Thr	Leu	
				770					775					780	
ACC	AGT	AAC	ATT	CCC	GAG	ATC	ACC	CCG	TTC	CTG	ATA	TTT	ATT	ATT	2385
Thr	Ser	Asn	Ile	Pro	Glu	Ile	Thr	Pro	Phe	Leu	Ile	Phe	Ile	Ile	
				785					790					795	
GCA	AAC	ATT	CCA	CTA	CCA	CTG	GGG	ACT	GTC	ACC	ATC	CTC	TGC	ATT	2430
Ala	Asn	Ile	Pro	Leu	Pro	Leu	Gly	Thr	Val	Thr	Ile	Leu	Cys	Ile	
				800					805					810	
GAC	TTG	GGC	ACT	GAC	ATG	GTT	CCT	GCC	ATC	TCC	CTG	GCT	TAT	GAG	2475
Asp	Leu	Gly	Thr	Asp	Met	Val	Pro	Ala	Ile	Ser	Leu	Ala	Tyr	Glu	
				815					820					825	
CAG	GCT	GAG	AGT	GAC	ATC	ATG	AAG	AGA	CAG	CCC	AGA	AAT	CCC	AAA	2520
Gln	Ala	Glu	Ser	Asp	Ile	Met	Lys	Arg	Gln	Pro	Arg	Asn	Pro	Lys	
				830					835					840	
ACA	GAC	AAA	CTT	GTG	AAT	GAG	CGG	CTG	ATC	AGC	ATG	GCC	TAT	GGG	2565
Thr	Asp	Lys	Leu	Val	Asn	Glu	Arg	Leu	Ile	Ser	Met	Ala	Tyr	Gly	
				845					850					855	
CAG	ATT	GGA	ATG	ATC	CAG	GCC	CTG	GGA	GGC	TTC	TTT	ACT	TAC	TTT	2610
Gln	Ile	Gly	Met	Ile	Gln	Ala	Leu	Gly	Gly	Phe	Phe	Thr	Tyr	Phe	
				860					865					870	
GTG	ATT	CTG	GCT	GAG	AAC	GGC	TTC	CTC	CCA	ATT	CAC	CTG	TTG	GGC	2655
Val	Ile	Leu	Ala	Glu	Asn	Gly	Phe	Leu	Pro	Ile	His	Leu	Leu	Gly	
				875					880					885	
CTC	CGA	GTG	GAC	TGG	GAT	GAC	CGC	TGG	ATC	AAC	GAT	GTG	GAA	GAC	2700
Leu	Arg	Val	Asp	Trp	Asp	Asp	Arg	Trp	Ile	Asn	Asp	Val	Glu	Asp	
				890					895					900	
AGC	TAC	GGG	CAG	CAG	TGG	ACC	TAT	GAG	CAG	AGG	AAA	ATC	GTG	GAG	2745
Ser	Tyr	Gly	Gln	Gln	Trp	Thr	Tyr	Glu	Gln	Arg	Lys	Ile	Val	Glu	
				905					910					915	
TTC	ACC	TGC	CAC	ACA	GCC	TTC	TTC	GTC	AGT	ATC	GTG	GTG	GTG	CAG	2790
Phe	Thr	Cys	His	Thr	Ala	Phe	Phe	Val	Ser	Ile	Val	Val	Val	Gln	
				920					925					930	
TGG	GCC	GAC	TTG	GTC	ATC	TGT	AAG	ACC	AGG	AGG	AAT	TCG	GTC	TTC	2835

Trp	Ala	Asp	Leu	Val	Ile	Cys	Lys	Thr	Arg	Arg	Asn	Ser	Val	Phe	
				935					940					945	
CAG	CAG	GGG	ATG	AAG	AAC	AAG	ATC	TTG	ATA	TTT	GGC	CTC	TTT	GAA	2880
Gln	Gln	Gly	Met	Lys	Asn	Lys	Ile	Leu	Ile	Phe	Gly	Leu	Phe	Glu	
				950					955					960	
GAG	ACA	GCC	CTG	GCT	GCT	TTC	CTT	TCC	TAC	TGC	CCT	GGA	ATG	GGT	2925
Glu	Thr	Ala	Leu	Ala	Ala	Phe	Leu	Ser	Tyr	Cys	Pro	Gly	Met	Gly	
				965					970					975	
GTT	GCT	CTT	AGG	ATG	TAT	CCC	CTC	AAA	CCT	ACC	TGG	TGG	TTC	TGT	2970
Val	Ala	Leu	Arg	Met	Tyr	Pro	Leu	Lys	Pro	Thr	Trp	Trp	Phe	Cys	
				980					985					990	
GCC	TTC	CCC	TAC	TCT	CTT	CTC	ATC	TTC	GTA	TAT	GAC	GAA	GTC	AGA	3015
Ala	Phe	Pro	Tyr	Ser	Leu	Leu	Ile	Phe	Val	Tyr	Asp	Glu	Val	Arg	
				995					1000					1005	
AAA	CTC	ATC	ATC	AGG	CGA	CGC	CCT	GGC	GGC	TGG	GTG	GAG	AAG	GAA	3060
Lys	Leu	Ile	Ile	Arg	Arg	Arg	Pro	Gly	Gly	Trp	Val	Glu	Lys	Glu	
				1010					1015					1020	
ACC	TAC	TAT													
Thr	Tyr	Tyr													

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:1023 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Lys	Gly	Val	Gly	Arg	Asp	Lys	Tyr	Glu	Pro	Ala	Ala	Val	
1				5					10					15	
Ser	Glu	Gln	Glu	Asp	Lys	Lys	Glu	Lys	Lys	Glu	Lys	Lys	Asp	Arg	
				20					25					30	
Asp	Met	Asp	Glu	Leu	Lys	Lys	Glu	Val	Ser	Met	Asp	Asp	His	Lys	
				35					40					45	
Leu	Ser	Leu	Asp	Glu	Leu	His	Arg	Lys	Tyr	Gly	Thr	Asp	Leu	Ser	
				50					55					60	
Arg	Gly	Leu	Thr	Ser	Ala	Arg	Ala	Ala	Glu	Ile	Leu	Ala	Arg	Asp	
				65					70					75	
Gly	Pro	Asn	Ala	Leu	Thr	Pro	Pro	Pro	Thr	Thr	Pro	Glu	Trp	Ile	
				80					85					90	
Lys	Phe	Cys	Arg	Gln	Leu	Phe	Gly	Gly	Phe	Ser	Met	Leu	Leu	Trp	
				95					100					105	
Ile	Gly	Ala	Ile	Leu	Cys	Phe	Leu	Ala	Tyr	Ser	Ile	Gln	Ala	Ala	
				110					115					120	
Thr	Glu	Glu	Glu	Pro	Gln	Asn	Asp	Asn	Leu	Tyr	Leu	Gly	Val	Val	
				125					130					135	

Leu	Ser	Ala	Val	Val	Ile	Ile	Thr	Gly	Cys	Phe	Ser	Tyr	Tyr	Gln	140	145	150
Glu	Ala	Lys	Ser	Ser	Lys	Ile	Met	Glu	Ser	Phe	Lys	Asn	Met	Val	155	160	165
Pro	Gln	Gln	Ala	Leu	Val	Ile	Arg	Asn	Gly	Glu	Lys	Met	Ser	Ile	170	175	180
Asn	Ala	Glu	Glu	Val	Val	Val	Gly	Asp	Lue	Val	Glu	Val	Lys	Gly	185	190	195
Gly	Asp	Arg	Ile	Pro	Ala	Asp	Leu	Arg	Ile	Ile	Ser	Ala	Asn	Gly	200	205	210
Cys	Lys	Val	Asp	Asn	Ser	Ser	Leu	Thr	Gly	Glu	Ser	Glu	Pro	Gln	215	220	225
Thr	Arg	Ser	Pro	Asp	Phe	Thr	Asn	Glu	Asn	Pro	Leu	Glu	Thr	Arg	230	235	240
Asn	Ile	Ala	Phe	Phe	Ser	Thr	Asn	Cys	Val	Glu	Gly	Thr	Ala	Arg	245	250	255
Gly	Ile	Val	Val	Tyr	Thr	Gly	Asp	Arg	Thr	Val	Met	Gly	Arg	Ile	260	265	270
Ala	Thr	Leu	Ala	Ser	Gly	Leu	Glu	Gly	Gly	Gln	Thr	Pro	Ile	Ala	275	280	285
Ala	Glu	Ile	Glu	His	Phe	Ile	His	Ile	Ile	Thr	Gly	Val	Ala	Val	290	295	300
Phe	Leu	Gly	Val	Ser	Phe	Phe	Ile	Leu	Ser	Leu	Ile	Leu	Glu	Tyr	305	310	315
Thr	Trp	Leu	Glu	Ala	Val	Ile	Phe	Leu	Ile	Gly	Ile	Ile	Val	Ala	320	325	330
Asn	Val	Pro	Glu	Gly	Leu	Leu	Ala	Thr	Val	Thr	Val	Cys	Leu	Thr	335	340	345
Leu	Thr	Ala	Lys	Arg	Met	Ala	Arg	Lys	Asn	Cys	Leu	Val	Lys	Asn	350	355	360
Leu	Glu	Ala	Val	Glu	Thr	Leu	Gly	Ser	Thr	Ser	Thr	Ile	Cys	Ser	365	370	375
Asp	Lys	Thr	Gly	Thr	Leu	Thr	Gln	Asn	Arg	Met	Thr	Val	Ala	His	380	385	390
Met	Trp	Phe	Asp	Asn	Gln	Ile	His	Glu	Ala	Asp	Thr	Thr	Glu	Asn	395	400	405
Gln	Ser	Gly	Val	Ser	Phe	Asp	Lys	Thr	Ser	Ala	Thr	Trp	Leu	Ala	410	415	420
Leu	Ser	Arg	Ile	Ala	Gly	Leu	Cys	Asn	Arg	Ala	Val	Phe	Gln	Ala	425	430	435

Asn	Gln	Glu	Asn	Leu	Pro	Ile	Leu	Lys	Arg	Ala	Val	Ala	Gly	Asp	440	445	450
Ala	Ser	Glu	Ser	Ala	Leu	Leu	Lys	Cys	Ile	Glu	Leu	Cys	Cys	Gly	455	460	465
Ser	Val	Lys	Glu	Met	Arg	Glu	Arg	Tyr	Ala	Lys	Ile	Val	Glu	Ile	470	475	480
Pro	Phe	Asn	Ser	Thr	Asn	Lys	Tyr	Gln	Leu	Ser	Ile	His	Lys	Asn	485	490	495
Pro	Asn	Thr	Ser	Glu	Pro	Gln	His	Leu	Leu	Val	Met	Lys	Gly	Ala	500	505	510
Pro	Glu	Arg	Ile	Leu	Asp	Arg	Cys	Ser	Ser	Ile	Leu	Leu	His	Gly	515	520	525
Lys	Glu	Gln	Pro	Leu	Asp	Glu	Glu	Leu	Lys	Asp	Ala	Phe	Gln	Asn	530	535	540
Ala	Tyr	Leu	Glu	Leu	Gly	Gly	Leu	Gly	Glu	Arg	Val	Leu	Gly	Phe	545	550	555
Cys	His	Leu	Phe	Leu	Pro	Asp	Glu	Gln	Phe	Pro	Glu	Gly	Phe	Gln	560	565	570
Phe	Asp	Thr	Asp	Asp	Val	Asn	Phe	Pro	Ile	Asp	Asn	Leu	Cys	Phe	575	580	585
Val	Gly	Leu	Ile	Ser	Met	Ile	Asp	Pro	Pro	Arg	Ala	Ala	Val	Pro	590	595	600
Asp	Ala	Val	Gly	Lys	Cys	Arg	Ser	Aal	Gly	Ile	Lys	Val	Ile	Met	605	610	615
Val	Thr	Gly	Asp	His	Pro	Ile	Thr	Ala	Lys	Ala	Ile	Ala	Lys	Gly	620	625	630
Val	Gly	Ile	Ile	Ser	Glu	Gly	Asn	Glu	Thr	Val	Glu	Asp	Ile	Ala	635	640	645
Ala	Arg	Leu	Asn	Ile	Pro	Val	Ser	Gln	Val	Asn	Pro	Arg	Asp	Ala	650	655	660
Lys	Ala	Cys	Val	Val	His	Gly	Ser	Asp	Leu	Lys	Asp	Met	Thr	Ser	665	670	675
Glu	Glm	Leu	Asp	Asp	Ile	Leu	Lys	Tyr	His	Thr	Glu	Ile	Val	Phe	680	685	690
Ala	Arg	Thr	Ser	Pro	Gln	Gln	Lys	Leu	Ile	Ile	Val	Glu	Gly	Cys	695	700	705
Gln	Arg	Gln	Gly	Ala	Ile	Val	Ala	Val	Thr	Gly	Asp	Gly	Val	Asn	710	715	720
Asp	Ser	Pro	Ala	Leu	Lys	Lys	Ala	Asp	Ile	Gly	Val	Ala	Met	Gly	725	730	735

Ile	Ala	Gly	Ser	Asp	Val	Ser	Lys	Gln	Ala	Ala	Asp	Met	Ile	Leu	740	745	750
Leu	Asp	Asp	Asn	Phe	Ala	Ser	Ile	Val	Thr	Gly	Val	Glu	Glu	Gly	755	760	765
Arg	Leu	Ile	Phe	Asp	Asn	Leu	Lys	Lys	Ser	Ile	Ala	Tyr	Thr	Leu	770	775	780
Thr	Ser	Asn	Ile	Pro	Glu	Ile	Thr	Pro	Phe	Leu	Ile	Phe	Ile	Ile	785	790	795
Ala	Asn	Ile	Pro	Leu	Pro	Leu	Gly	Thr	Val	Thr	Ile	Leu	Cys	Ile	800	805	810
Asp	Leu	Gly	Thr	Asp	Met	Val	Pro	Ala	Ile	Ser	Leu	Ala	Tyr	Glu	815	820	825
Gln	Ala	Glu	Ser	Asp	Ile	Met	Lys	Arg	Gln	Pro	Arg	Asn	Pro	Lys	830	835	840
Thr	Asp	Lys	Leu	Val	Asn	Glu	Arg	Leu	Ile	Ser	Met	Ala	Tyr	Gly	845	850	855
Gln	Ile	Gly	Met	Ile	Gln	Ala	Leu	Gly	Gly	Phe	Phe	Thr	Tyr	Phe	860	865	870
Val	Ile	Leu	Ala	Glu	Asn	Gly	Phe	Leu	Pro	Ile	His	Leu	Leu	Gly	875	880	885
Leu	Arg	Val	Asp	Trp	Asp	Asp	Arg	Trp	Ile	Asn	Asp	Val	Glu	Asp	890	895	900
Ser	Tyr	Gly	Gln	Gln	Trp	Thr	Tyr	Glu	Gln	Arg	Lys	Ile	Val	Glu	905	910	915
Phe	Thr	Cys	His	Thr	Ala	Phe	Phe	Val	Ser	Ile	Val	Val	Val	Gln	920	925	930
Trp	Ala	Asp	Leu	Val	Ile	Cys	Lys	Thr	Arg	Arg	Asn	Ser	Val	Phe	935	940	945
Gln	Gln	Gly	Met	Lys	Asn	Lys	Ile	Leu	Ile	Phe	Gly	Leu	Phe	Glu	950	955	960
Glu	Thr	Ala	Leu	Ala	Ala	Phe	Leu	Ser	Tyr	Cys	Pro	Gly	Met	Gly	965	970	975
Val	Ala	Leu	Arg	Met	Tyr	Pro	Leu	Lys	Pro	Thr	Trp	Trp	Phe	Cys	980	985	990
Ala	Phe	Pro	Tyr	Ser	Leu	Leu	Ile	Phe	Val	Tyr	Asp	Glu	Val	Arg	995	1000	1005
Lys	Leu	Ile	Ile	Arg	Arg	Arg	Pro	Gly	Gly	Trp	Val	Glu	Lys	Glu	1010	1015	1020
Thr	Tyr	Tyr															

(2) INFORMATION FOR SEQ ID NO:7:

(I) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 909 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG	GCC	CGC	GGG	AAA	GCC	AAG	GAG	GAG	GGC	AGC	TGG	AAG	AAA	TTC	45
Met	Ala	Arg	Gly	Lys	Ala	Lys	Glu	Glu	Gly	Ser	Trp	Lys	Lys	Phe	
1				5					10					15	
ATC	TGG	AAC	TCA	GAG	AAG	AAG	GAG	TTT	CTG	GGC	AGG	ACC	GGT	GGC	90
Ile	Trp	Asn	Ser	Glu	Lys	Lys	Glu	Phe	Leu	Gly	Arg	Thr	Gly	Gly	
				20					25					30	
AGT	TGG	TTT	AAG	ATC	CTT	CTA	TTC	TAC	GTA	ATA	TTT	TAT	GGC	TGC	135
Ser	Trp	Phe	Lys	Ile	Leu	Leu	Phe	Tyr	Val	Ile	Phe	Tyr	Gly	Cys	
				35					40					45	
CTG	GCT	GGC	ATC	TTC	ATC	GGA	ACC	ATC	CAA	GTG	ATG	CTG	CTC	ACC	180
Leu	Ala	Gly	Ile	Phe	Ile	Gly	Thr	Ile	Gln	Val	Met	Leu	Leu	Thr	
				50					55					60	
ATC	AGT	GAA	TTT	AAG	CCC	ACA	TAT	CAG	GAC	CGA	GTG	GCC	CCG	CCA	225
Ile	Ser	Glu	Phe	Lys	Pro	Thr	Tyr	Gln	Asp	Arg	Val	Ala	Pro	Pro	
				65					70					75	
GGA	TTA	ACA	CAG	ATT	CCT	CAG	ATC	CAG	AAG	ACT	GAA	ATT	TCC	TTT	270
Gly	Leu	Thr	Gln	Ile	Pro	Gln	Ile	Gln	Lys	Thr	Glu	Ile	Ser	Phe	
				80					85					90	
CGT	CCT	AAT	GAT	CCC	AAG	AGC	TAT	GAG	GCA	TAT	GTA	CTG	AAC	ATA	315
Arg	Pro	Asn	Asp	Pro	Lys	Ser	Tyr	Glu	Ala	Tyr	Val	Leu	Asn	Ile	
				95					100					105	
GTT	AGG	TTC	CTG	GAA	AAG	TAC	AAA	GAT	TCA	GCC	CAG	AGG	GAT	GAC	360
Val	Arg	Phe	Leu	Glu	Lys	Tyr	Lys	Asp	Ser	Ala	Gln	Arg	Asp	Asp	
				110					115					120	
ATG	ATT	TTT	GAA	GAT	TGT	GGC	GAT	GTG	CCC	AGT	GAA	CCG	AAA	GAA	405
Met	Ile	Phe	Glu	Asp	Cys	Gly	Asp	Val	Pro	Ser	Glu	Pro	Lys	Glu	
				125					130					135	
CGA	GGA	GAC	TTT	AAT	CAT	GAA	CGA	GGA	GAG	CGA	AAG	GTC	TGC	AGA	450
Arg	Gly	Asp	Phe	Asn	His	Glu	Arg	Gly	Glu	Arg	Lys	Val	Cys	Arg	
				140					145					150	
TTC	AAG	CTT	GAA	TGG	CTG	GGA	AAT	TGC	TCT	GGA	TTA	AAT	GAT	GAA	495
Phy	Lys	Leu	Glu	Trp	Leu	Gly	Asn	Cys	Ser	Gly	Leu	Asn	Asp	Glu	
				155					160					165	
ACT	TAT	GGC	TAC	AAA	GAG	GGC	AAA	CCG	TGC	ATT	ATT	ATA	AAG	CTC	540
Thr	Tyr	Gly	Tyr	Lys	Glu	Gly	Lys	Pro	Cys	Ile	Ile	Ile	Lys	Leu	
				170					175					180	
AAC	CGA	GTT	CTA	GGC	TTC	AAA	CCT	AAG	CCT	CCC	AAG	AAT	GAG	TCC	585
Asn	Arg	Val	Leu	Gly	Phe	Lys	Pro	Lys	Pro	Pro	Lys	Asn	Glu	Ser	
				185					190					195	
TTG	GAG	ACT	TAC	CCA	GTG	ATG	AAG	TAT	AAC	CCA	AAT	GTC	CTT	CCC	630
Leu	Glu	Thr	Tyr	Pro	Val	Met	Lys	Tyr	Asn	Pro	Asn	Val	Leu	Pro	

	200	205	210	
GTT CAG TGC ACT	GGC AAG CGA GAT GAA	GAT AAG GAT AAA GTT	GGA	675
Val Gln Cys Thr	Gly Lys Arg Asp Glu	Asp Lys Asp Lys Val	Gly	
	215	220	225	
AAT GTG GAG TAT	TTT GGA CTG GGC AAC	TCC CCT GGT TTT CCT	CTG	720
Asn Val Glu Tyr	Phe Gly Leu Gly Asn	Ser Pro Gly Phe Pro	Leu	
	230	235	240	
CAG TAT TAT CCG	TAC TAT GGC AAA CTC	CTG CAG CCC AAA TAC	CTG	765
Gln Tyr Tyr Pro	Tyr Tyr Gly Lys Leu	Leu Gln Pro Lys Tyr	Leu	
	245	250	255	
CAG CCC CTG CTG	GCC GTA CAG TTC ACC	AAT CTT ACC ATG GAC	ACT	810
Gln Pro Leu Leu	Ala Val Gln Phe Thr	Asn Leu Thr Met Asp	Thr	
	260	265	270	
GAA ATT CGC ATA	GAG TGT AAG GCG TAC	GGT GAG AAC ATT GGG	TAC	855
Glu Ile Arg Ile	Glu Cys Lys Ala Tyr	Gly Glu Asn Ile Gly	Tyr	
	275	280	285	
AGT GAG AAA GAC	CGT TTT CAG GGA CGT	TTT GAT GTA AAA ATT	GAA	900
Ser Glu Lys Asp	Arg Phe Gln Gly Arg	Phe Asp Val Lys Ile	Glu	
	290	295	300	
GTT AAG AGC	909			
Val Lys Ser				

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Arg	Gly	Lys	Ala	Lys	Glu	Glu	Gly	Ser	Trp	Lys	Lys	Phe
1				5					10					15
Ile	Trp	Asn	Ser	Glu	Lys	Lys	Glu	Phe	Leu	Gly	Arg	Thr	Gly	Gly
				20					25					30
Ser	Trp	Phe	Lys	Ile	Leu	Leu	Phe	Tyr	Val	Ile	Phe	Tyr	Gly	Cys
				35					40					45
Leu	Ala	Gly	Ile	Phe	Ile	Gly	Thr	Ile	Gln	Val	Met	Leu	Leu	Thr
				50					55					60
Ile	Ser	Glu	Phe	Lys	Pro	Thr	Tyr	Gln	Asp	Arg	Val	Ala	Pro	Pro
				65					70					75
Gly	Leu	Thr	Gln	Ile	Pro	Gln	Ile	Gln	Lys	Thr	Glu	Ile	Ser	Phe
				80					85					90
Arg	Pro	Asn	Asp	Pro	Lys	Ser	Tyr	Glu	Ala	Tyr	Val	Leu	Asn	Ile
				95					100					105
Val	Arg	Phe	Leu	Glu	Lys	Tyr	Lys	Asp	Ser	Ala	Gln	Arg	Asp	Asp
				110					115					120

Met	Ile	Phe	Glu	Asp	Cys	Gly	Asp	Val	Pro	Ser	Glu	Pro	Lys	Glu	125	130	135
Arg	Gly	Asp	Phe	Asn	His	Glu	Arg	Gly	Glu	Arg	Lys	Val	Cys	Arg	140	145	150
Phy	Lys	Leu	Glu	Trp	Leu	Gly	Asn	Cys	Ser	Gly	Leu	Asn	Asp	Glu	155	160	165
Thr	Tyr	Gly	Tyr	Lys	Glu	Gly	Lys	Pro	Cys	Ile	Ile	Ile	Lys	Leu	170	175	180
Asn	Arg	Val	Leu	Gly	Phe	Lys	Pro	Lys	Pro	Pro	Lys	Asn	Glu	Ser	185	190	195
Leu	Glu	Thr	Tyr	Pro	Val	Met	Lys	Tyr	Asn	Pro	Asn	Val	Leu	Pro	200	205	210
Val	Gln	Cys	Thr	Gly	Lys	Arg	Asp	Glu	Asp	Lys	Asp	Lys	Val	Gly	215	220	225
Asn	Val	Glu	Tyr	Phe	Gly	Leu	Gly	Asn	Ser	Pro	Gly	Phe	Pro	Leu	230	235	240
Gln	Tyr	Tyr	Pro	Tyr	Tyr	Gly	Lys	Leu	Leu	Gln	Pro	Lys	Tyr	Leu	245	250	255
Gln	Pro	Leu	Leu	Ala	Val	Gln	Phe	Thr	Asn	Leu	Thr	Met	Asp	Thr	260	265	270
Glu	Ile	Arg	Ile	Glu	Cys	Lys	Ala	Tyr	Gly	Glu	Asn	Ile	Gly	Tyr	275	280	285
Ser	Glu	Lys	Asp	Arg	Phe	Gln	Gly	Arg	Phe	Asp	Val	Lys	Ile	Glu	290	295	300
Val	Lys	Ser															

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGGAAGG GGGTTGGACG TGAT 24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAGTAGGTT TCCTTCTCCA CCCA 24

(2) INFORMATION FOR SEQ ID NO:11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGCCCGCG GGAAAGCCAA GGAG 24

(2) INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTCTTAACT TCAATTTTTC CATC 24